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LOCUS
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Sequence 1 from Patent WO2004026772.
ACCESSION
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VERSION
CQ796908.1 GI:46408534
KEYWORDS
SOURCE
unidentified
ORGANISM
unclassified sequences.
REFERENCE
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AUTHORS
Hovanec, T. A.
TITLES
Ammonia-oxidizing bacteria and methods of using and detecting
JOURNAL
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Patent: WO 2004026772-A 1 01-APR-2004;
AquaRIA Inc. (US)
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Best Local Similarity 100.0%; Pred. No. 8.3e-16;
Matches 1457; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1381 GGGAGTGGGTTTCAACAGAGAGGTAGCTTAACCGTAAGAGAGGCGCTTGCCACGGTGA 1440
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QY      1441 GATTGATGACTGGGGTG 1457
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ACCESSION CS089154  
VERSION CS089154.1 GI:66714438  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1  
AUTHORS Hovanec, T. A. and Burrell, P. C.  
TITLE Ammonia-oxidizing bacteria  
JOURNAL Patent: EP 1502948-A 1 02-FEB-2005;  
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Query Match 100.0%; Score 1457; DB 6; Length 1457;  
Best Local Similarity 100.0%; Pred. No. 8.3e-16;  
Matches 1457; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 AUTHORS Hovanec, T.A. and Burrell, P.C.  
 TITLE Ammonia-oxidizing bacteria  
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 Best Local Similarity 100.0%; Pred. No. 8.3e-16;  
 Matches 1457; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTGAACGCTGGCGGAGCTTTACATGCAAGTCGAACGGCGAGAGGATGCTTGCAAT 60  
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| Query      | Match   | 100.0%   | Score 1457 | DB 6   | Length 1457     |
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| Db         | 901   | GCACAGCGGTGATTATGTGGATTAAATTCGATGCAACGGGAAAACTTACTTACCTT     | 960        |        |                 |
| Qy         | 961   | GACATGTAGCGAATTTTCTAGAGATAGATTAGTCTTGGGAGCGCTAACAGGTGCTG     | 1020       |        |                 |
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| Db         | 1021  | CATGGCTGTCCGTCAAGCTGTGTCTGAGATGTGGGTTAAAGTCCCGACAGCGCAAC     | 1080       |        |                 |
| Qy         | 1081  | CTGTCTATTAAATTTGCAATCTTATTTGGTGGGCACTTTAATGAGACTGCGGTGACAAAC | 1140       |        |                 |
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| Db         | 1141  | GAGGAAGGTGGGGAGTAGTCGCAAGCTCATGGCCCTTAATGGGTGAGGCTTCAACGTAA  | 1200       |        |                 |
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| Qy         | 1261  | TCGTAGTCCGAGTCCGAGTCTTGCAACTCGACTCCGTGAAGTGGTAATGCTAGTAATGC  | 1320       |        |                 |
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| Db         | 1381  | GGGAGTGGGTTTACACAGAGCGGTAGTCTTAACGTAAGAGGCGCTTGGCACGCTGA     | 1440       |        |                 |
| Qy         | 1441  | GATTCATGACTGGGGTG 1457                                       |            |        |                 |
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| DEFINITION | Sequence 1 from Patent WO0190312.                         |  |            |        |                 |
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| VERSION    | AXJ16092.1  | GI:17899283  |            |        |                 |
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| SOURCE     | unidentified  |  |            |        |                 |
| ORGANISM   | unclassified  |  |            |        |                 |
| REFERENCE  | 1   |  |            |        |                 |
| AUTHORS    | Hovaneec, T. A. and Burrell, P. C.                        |  |            |        |                 |
| TITLE      | Ammonia-oxidizing bacteria                                |  |            |        |                 |
| JOURNAL    | Patent: WO 0190312-A 1 29-NOV-2001;                       |  |            |        |                 |
| FEATURES   | FEATURES  |  |            |        |                 |
| source     | location/Qualifiers                                       |  |            |        |                 |
|            | 1. 1457   |  |            |        |                 |
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|            | /db_xref="taxon:32644"                                    |  |            |        |                 |
|            | /note="AOB Type A ammonia-oxidizing bacterium represented |  |            |        |                 |
|            | by R7 clone140"   |  |            |        |                 |
| ORIGIN     |   |  |            |        |                 |

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| Best Local Similarity 100.0%; Pred. No. 8,3e-16;              |   |      |
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| Db  | 1 ATTGAACGCTGGCGGCACTGCTTTACACATGCAGTGAACGGCAGCAGCATGCTTGCAAT       | 60   |
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| Db  | 61 CTGTGTGCGAGTGGCCGGAACGGGTGAGTAATGCAATCCGAACGTATCCAGAAAGAGGGGGGTA | 120  |
| QY  | 121 ACCGATCGAAAGATGTGTCTAATACCGCATATCTTAAGAGGAAAGCAGGGGATCGAAA      | 180  |
| Db  | 121 ACCGATCGAAAGATGTGTCTAATACCGCATATCTTAAGAGGAAAGCAGGGGATCGAAA      | 180  |
| QY  | 181 GACCTTTCGCTTTTGGAGCGGCGCATGTCTGATTAGCTAGTTGGTGGGGTAAAGGCTTAC    | 240  |
| Db  | 181 GACCTTTCGCTTTTGGAGCGGCGCATGTCTGATTAGCTAGTTGGTGGGGTAAAGGCTTAC    | 240  |
| QY  | 241 CAAGCGCAGCATCAGTATGTTGTGTCTGAGAGGACGACGACGACATCTGGGACTGAGACAGC  | 300  |
| Db  | 241 CAAGCGCAGCATCAGTATGTTGTGTCTGAGAGGACGACGACGACATCTGGGACTGAGACAGC  | 300  |
| QY  | 301 GCCCAGACTCTCTACGGGAGCAGCAGTGGGGAAATTTTGGCAATGGCGCAGACGCTGATC    | 360  |
| Db  | 301 GCCCAGACTCTCTACGGGAGCAGCAGTGGGGAAATTTTGGCAATGGCGCAGACGCTGATC    | 360  |
| QY  | 361 CAGCAATGCCGCTGACTGAAGAAAGGCTTCGGGTGTAAAGCTCTTTCACTGAGAAAGA      | 420  |
| Db  | 361 CAGCAATGCCGCTGACTGAAGAAAGGCTTCGGGTGTAAAGCTCTTTCACTGAGAAAGA      | 420  |
| QY  | 421 AAAGGTACGGTAAATATGTGTGATCTGATACGGTATCCAGAAAGAAAGCAGCGGCTTAC     | 480  |
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| QY  | 481 TAGGTGCACAGCGCGGTAAATACGTAGGGGTGCAAGCGTTAATCCGAATTTACTCGGGCGT   | 540  |
| Db  | 481 TAGGTGCACAGCGCGGTAAATACGTAGGGGTGCAAGCGTTAATCCGAATTTACTCGGGCGT   | 540  |
| QY  | 541 AAAGGTGCGCAGCGGCTTTGTAAAGTCAGATGTGAATCCCGGGGCTTAACTGGGAAT       | 600  |
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| QY  | 601 TGCCTTTGAAACTACAAAGCTGATGATGTGGCAGAGGAGGTGGAATTCATGTGTAGAG      | 660  |
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| Db  | 661 TGAATATCCGTAGATATGGAAGAACTATCATGATGCCAAGGACAGCTCTCGGGTTAAACT    | 720  |
| QY  | 721 GAGCCTCATGCACGAAGAGCTGGGGAGCAAAACAGATTTAGATACCTGTGTAGTCAAGCC    | 780  |
| Db  | 721 GAGCCTCATGCACGAAGAGCTGGGGAGCAAAACAGATTTAGATACCTGTGTAGTCAAGCC    | 780  |
| QY  | 781 CTAAACGATGCAACTAGTTGTTGGGCTTATTAGCTTGGTAAAGAACTTAACGCTGA        | 840  |
| Db  | 781 CTAAACGATGCAACTAGTTGTTGGGCTTATTAGCTTGGTAAAGAACTTAACGCTGA        | 840  |
| QY  | 841 AGTTGACCCGCTGGGGAGTACGGTTCGGAATTTAACTAAAGGAATTGACGGGGAGCC       | 900  |
| Db  | 841 AGTTGACCCGCTGGGGAGTACGGTTCGGAATTTAACTAAAGGAATTGACGGGGAGCC       | 900  |
| QY  | 901 GCACAAAGCGGTGATATATGTGATTAATTTGATGCAACGCGAATACTTACTACCTT        | 960  |
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LOCUS AXJ16093  
DEFINITION Sequence 2 from Patent WO0190312.  
ACCESSION AXJ16093  
VERSION AXJ16093.1 GI:17899284

KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1  
unclassified sequences.

AUTHORS Hovanes, T.A. and Burrell, P.C.  
TITLE Ammonia-oxidizing bacteria  
JOURNAL Patent: WO 0190312-A 2 25-NOV-2001;  
AQUARIA, Inc. (US)

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/note="AOB Type A1 ammonia-oxidizing bacterium represented  
by R7 clone187"

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Query Match 100.0%; Score 1457; DB 6; Length 1457;  
Best Local Similarity 100.0%; Pred. No. 8.3e-16;  
Matches 1457; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS Nitrosomonas sp. R7c131 16S ribosomal RNA gene, partial sequence.  
DEFINITION AF386752  
ACCESSION AF386752 GI:17864829  
VERSION ENV.  
KEYWORDS Nitrosomonas sp. R7c131  
SOURCE Nitrosomonas sp. R7c131  
ORGANISM Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;  
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REFERENCE 1 (bases 1 to 1457)  
Burrell, P.C., Phalen, C.M. and Hovanec, T.A.  
Identification of bacteria responsible for ammonia oxidation in  
freshwater aquaria  
Appl. Environ. Microbiol. 67 (12), 5791-5800 (2001)  
JOURNAL 11722936  
PUBMED 2 (bases 1 to 1457)  
REFERENCE Burrell, P.C., Phalen, C.M. and Hovanec, T.A.  
AUTHORS Direct Submission  
TITLE Submitted (30-MAY-2001) Aquatic Research Laboratory, The Aquaria  
JOURNAL Group, 6100 Condon Dr. Moorpark, CA 93021, USA  
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VERSION       CQ796909.1 GI:46408535
KEYWORDS
SOURCE        unidentified
ORGANISM      unidentified
REFERENCE     1.
AUTHORS       Hovanec, T. A.
TITLE         Ammonia-oxidizing bacteria and methods of using and detecting
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Query Match      99.7%; Score 1457.2; DB 6; Length 1457;
Beet Local Similarity 99.8%; Pred. No. 9.8e-16;
Matches 1454; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy      1261 TCGTAGTCGGATCGAGTCTGCAACTGACTCCGTGAAGTGGAAATCGCTAGTAATCCG 1320
Db      1261 TCGTAGTCGGATCGAGTCTGCAACTGACTCCGTGAAGTGGAAATCGCTAGTAATCCG 1320
Qy      1321 GGATCAGCATGTGCGGGTGAATACGTTCCGGGCTTTGTAACACACCGCCGTCACACAT 1380
Db      1321 GGATCAGCATGTGCGGGTGAATACGTTCCGGGCTTTGTAACACACCGCCGTCACACAT 1380
Qy      1381 GGGAGTGGTTTCAACAGAGAGGTAGCTTAACGTAAGAGAGGCGCTTGGCACGAGTGA 1440
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RESULT 9
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LOCUS        Nitrosomonas sp. R7c187 16S ribosomal RNA gene, partial sequence.
DEFINITION   AF386757
ACCESSION    AF386757.1 GI:17864834
VERSION      ENV.
KEYWORDS     Nitrosomonas sp. R7c187
SOURCE       Nitrosomonas sp. R7c187
ORGANISM     Nitrosomonas sp. R7c187

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Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales; Nitrosomonadaceae; Nitrosomonas; environmental samples.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
PUBMED  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
SOURCE

1 (bases 1 to 1457)  
Burrell, P.C., Phalen, C.M. and Hovanec, T.A.  
Identification of bacteria responsible for ammonia oxidation in freshwater aquaria  
Appl. Environ. Microbiol. 67 (12), 5791-5800 (2001)  
1172936

2 (bases 1 to 1457)  
Burrell, P.C., Phalen, C.M. and Hovanec, T.A.  
Direct Submission  
Submitted (30-MAY-2001) Aquatic Research Laboratory, The Aquaria Group, 6100 Condon Dr., Moorpark, CA 93021, USA  
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Query Match 99.5%; Score 1449; DB 3; Length 1457;  
Best Local Similarity 99.7%; Pred. No. 1.1e-15;  
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DEFINITION Nitrosomonas sp. R7c155 16S ribosomal RNA gene, partial sequence.  
ACCESSION AF386751  
VERSION AF386751.1 GI:17864828  
KEYWORDS ENV.  
SOURCE Nitrosomonas sp. R7c155  
ORGANISM Nitrosomonas sp. R7c155  
REFERENCE  
AUTHORS Burrell, P.C., Phalen, C.M. and Hovanec, T.A.  
TITLE Identification of bacteria responsible for ammonia oxidation in freshwater aquaria

JOURNAL Appl. Environ. Microbiol. 67 (12), 5791-5800 (2001)  
 PUBMED 11722936  
 REFERENCE 2 (bases 1 to 1426)  
 AUTHORS Burrell, P.C., Phalen, C.M. and Hovanec, T.A.  
 TITLE Direct Submission  
 JOURNAL Submitted (30-MAY-2001) Aquatic Research Laboratory, The Aquaria Group, 6100 Condon Dr., Moorpark, CA 93021, USA  
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 361 GGGTGTAAAGCTCTTCACTGACGAGAAAGAGTTACGGTAAATATCGTCACTCATGA 420  
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 DEFINITION AF386746  
 ACCESSION AF386746.1 GI:17864823  
 VERSION  
 KEYWORDS ENV.  
 SOURCE Nitrosomonas sp. Bf16c57  
 ORGANISM Nitrosomonas sp. Bf16c57  
 Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;  
 Nitrosomonadaceae; Nitrosomonas; environmental samples.  
 REFERENCE 1 (bases 1 to 1487)  
 AUTHORS Burrell, P.C., Phalen, C.M. and Hovanec, T.A.  
 TITLE Identification of bacteria responsible for ammonia oxidation in  
 freshwater aquaria  
 JOURNAL Appl. Environ. Microbiol. 67 (12), 5791-5800 (2001)  
 PUBMED 11722936  
 REFERENCE 2 (bases 1 to 1487)  
 AUTHORS Burrell, P.C., Phalen, C.M. and Hovanec, T.A.  
 TITLE Direct Submission  
 JOURNAL Submitted (30-MAY-2001) Aquatic Research Laboratory, The Aquaria Group, 6100 Condon Dr., Moorpark, CA 93021, USA  
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Best Local Similarity 97.6%; Pred. No. 8.5e-15;
Matches 1423; Conservative 0; Mismatches 34; Indels 1; Gaps 1;

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## RESULT 12

CQ796927

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

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Best Local Similarity 97.6%; Pred. No. 8.5e-15;
Matches 1423; Conservative 0; Mismatches 34; Indels 1; Gaps 1;

QY 1 ATTGAACGCTGGCGGCGATGCTTTACACATGCAAGTGCAGCGACGCGATGCTTGCAAT 60
DB 18 ATTGAACGCTGGCGGCGATGCTTTACACATGCAAGTGCAGCGACGCGATGCTTGCAAT 77

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ACCESSION AJ621032.1 GI:40994851
VERSION 16S ribosomal RNA, 16S rRNA gene.
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SOURCE Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
ORGANISM Nitrosomonadaceae; Nitrosomonas.

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REFERENCE 1
AUTHORS Bollmann, A., Schmidt, I. and Bodelier, P.L.E.
TITLE Influence of salt on activity, growth, protein pattern and fatty
acid composition of the new isolated ammonia oxidizing strain
Nitrosomonas strain Is343
Unpublished
2 (bases 1 to 1445)

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JOURNAL Direct Submission
REFERENCE Submitted (15-JAN-2004) Bollmann A., Department for Microbial
AUTHORS Ecology, NIOO-KNAW Centre for Limnology, Rijksstraatweg 6, 3631 AC
JOURNAL Nieuwersluis, NETHERLANDS

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 AUTHORS 1 (bases 1 to 1450)  
 Purkhold, U., Pommerening-Rose, A., Juretschko, S., Schmid, M.C.,  
 Koops, H.P. and Wagner, M.  
 TITLE Phylogeny of all recognized species of ammonia oxidizers based on  
 comparative 16S rRNA and amoA sequence analysis: implications for  
 molecular diversity surveys  
 JOURNAL Appl. Environ. Microbiol. 66 (12), 5368-5382 (2000)  
 PUBMED 11097916  
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 AUTHORS 2 (bases 1 to 1450)  
 Purkhold, U., Pommerening-Rose, A., Juretschko, S., Schmid, M.C.,  
 Koops, H.P. and Wagner, M.  
 TITLE Direct Sublesion  
 JOURNAL Submitted (26-MAY-2000) Lehrstuhl fuer Mikrobiologie, Technische  
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REFERENCE Purkhold, U., Pommerening-Roser, A., Juretschko, S., Schmid, M.C.,
AUTHORS Koops, H.P. and Wagner, M.
TITLE Phylogeny of all recognized species of ammonia oxidizers based on
comparative 16S rRNA and amoA sequence analysis: implications for
molecular diversity surveys
JOURNAL Appl. Environ. Microbiol. 66 (12), 5368-5382 (2000)
PUBMED 11057916
REFERENCE Purkhold, U., Pommerening-Roser, A., Juretschko, S., Schmid, M.C.,
AUTHORS Koops, H.P. and Wagner, M.
TITLE Direct Submission
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Universitaet Muenchen, Am Hochanger 4, Freising 85350, Germany
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Db      ||||| 1394 AAGCGGTGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1453
Qy      ||||| 892 CGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 951
Db      ||||| 1454 CGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1513
Qy      ||||| 952 CCTAACCTTGATCAT -GTAGCGAAATTTTCTAAGAGATGATGATGATGATGATGATGATGATG 1010
Db      ||||| 1514 CCAAGCTTGTGACATCTGCTGCTATCTTCTAAGATGATGATGATGATGATGATGATGATGATGATG 1573
Qy      ||||| 1011 ACGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1070
Db      ||||| 1574 ACGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1633
Qy      ||||| 1071 GAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1130

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Db      ||||| 1634 GAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1693
Qy      ||||| 1131 TGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1190
Db      ||||| 1694 TGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1753
Qy      ||||| 1191 TGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1250
Db      ||||| 1754 ACGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1813
Qy      ||||| 1251 AGAAGCGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1310
Db      ||||| 1814 TTAAAGCATTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1873
Qy      ||||| 1311 TAGTAATCGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1370
Db      ||||| 1874 TAGTAATCGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1933
Qy      ||||| 1371 GTACACCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1430
Db      ||||| 1934 GTACACCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1993
Qy      ||||| 1431 GCCACGCTGAGATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1497
Db      ||||| 1994 CTTAAGTAAAGACCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2020

RESULT 2
LOCUS      CX109203
DEFINITION sative (indica cultivar-group) cDNA clone E1051022, E1053308, E1008B17, B1076L19, B1154A06, B1133B10, E111 5', mRNA sequence.
ACCESSION CX109203
VERSION    CX109203.1 GI:66922355
KEYWORDS   EST.
SOURCE      Oryza sativa (indica cultivar-group)
ORGANISM   Oryza sativa (indica cultivar-group)
REFERENCE   1 (bases 1 to 1954)
AUTHORS     Zhang,J., Feng,Q., Jin,C., Qiu,D., Zhang,L., Xie,K., Yuan,D., Han,B., Zhang,Q. and Wang,S.
TITLE       Features of the expressed sequences revealed by a large-scale analysis of ESTs from a normalized cDNA library of the elite indica rice cultivar Minghui 63
JOURNAL     Plant J. 42 (5), 772-780 (2005)
PUBMED     15918889
COMMENT     Contact: Wang S
            National Key Laboratory of Crop Genetic Improvement
            Huazhong Agricultural University
            Wuhan 430070, China
            Tel: 86-27-87282044
            Fax: 86-27-87287092
            Email: shpingwang@hotmail.com
            Seq primer: 17:
            Location/Qualifiers
            1..1954
            /organism="Oryza sativa (indica cultivar-group)"
            /mol_type="mRNA"
            /strain="indica"
            /cultivar="Minghui 63"
            /db_xref="taxon:39946"
            /clone="E1051022, E1053308, E1008B17, B1076L19, B1154A06, B1133B10, E111"
            /tissue_type="whole plant"
            /dev_stage="whole-life-cycle"
            /lab_host="E. coli DH10B"
            /clone_lib="A normalized whole-life-cycle cDNA library of rice"
            /note="Vector: pSPORT1, Site 1: SalI, Site 2: NotI; The library is constructed based on the strategy of saturation

```



## ORIGIN

hybridization with genomic DNA using rice cultivar Minghui 63. This library consists of cDNA from 15 directionally cloned cDNA libraries constructed with different tissues from 9 developmental stages."

Query Match 49.4%; Score 720.4; DB 8; Length 1954;  
 Best Local Similarity 73.1%; Pred. No. 5.9e-211;  
 Matches 1069; Conservative 0; Mismatches 336; Indels 57; Gaps 9;

3 TGAACGCTGGCGGCGATCTTACACATGCAAGCAACGCGAGCAGCGATCTTGCATCT 62  
 130 TGAACGCTGGCGGCGATCTTACACATGCAAGCAACGCGAGCAGCGATCTTGCATCT 177  
 63 GGTGGCAGATGGCGGCGGCGATCTTACATGCAAGCAACGCGAGCAGCGATCTTGCATCT 122  
 178 GTTTCAGATGGCGGCGGCGATCTTACATGCAAGCAACGCGAGCAGCGATCTTGCATCT 236  
 123 GCATCGAAGATGCTAATACCGCATTAATCTTAAGAGGAAAGCAGGCGATCGAAGA 182  
 237 AACTGGAACGCTTCTTAATACCGCATTAATCTTAAAGAGGAAAGCAGGCGATCGAAGA 283  
 183 CTTGCGCTTTTGGAGCGGCGGATCTTACATGCAAGCAACGCGAGCAGCGATCTTGCATCT 242  
 284 AATTCGCGGCGGCGGCGGCGATCTTACATGCAAGCAACGCGAGCAGCGATCTTGCATCT 343  
 243 AGGCGAGATCAATGATGTTGCTTGAAGAGCAGCAGCAGCAGCTGGGAGCTGAAGACGCG 302  
 344 AGGCGAGATCAATGATGTTGCTTGAAGAGCAGCAGCAGCAGCTGGGAGCTGAAGACGCG 403  
 303 CCGAGCTCTTACCGGAGGCGGAGCAGATGTTTGAAGCAATGGGCGGAGCAGCTGATCA 362  
 404 CCGAGCTCTTACCGGAGGCGGAGCAGATGTTTGAAGCAATGGGCGGAGCAGCTGATCA 463  
 363 GCATGCGCGGCTGATGAAGAGCCTTCCGGTGTGAAGCTCTTTCAGTGAAGAGAA 422  
 464 GCATGCGCGGCTGATGAAGAGCCTTCCGGTGTGAAGCTCTTTCAGTGAAGAGAA 523  
 423 AGCTTACGTTAATATGCTGATCTCATGACGCTATCGACAGAGAGAGCAGCGCTAATCA 482  
 524 -----CAATGACGCTTCTGAGAGAAATGAGATCGGCTAATCTC 560  
 483 CGTGGCAGAGCGCGGCTTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 542  
 561 TGTGCCAGAGCGCGGCTTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 620  
 543 AGGCTGCGAGCGCGCTTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 602  
 621 AGCTTCTGATGAGGCTTTTCAAGTCCGCTCAATCCAGGAGCTCAACCTGAGACAG 680  
 603 CGTTGAACTCAAGGCTAGAGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 662  
 681 CGGTGAACTCAAGGCTAGAGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 740  
 663 AATGCTGAGAGATGAGAGAAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 722  
 741 AATGCTGAGAGATGAGAGAAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 800  
 723 CGCTCATGACAGAGGCTGGGAGAGCAACAGATTAGATCCCTG--TAGTCCAGCGC 780  
 801 CACTGAGAGAGAGAGTATGAGGAGAGCAAAATGAGATTAAGAGCCCAAGTATTCATAGCC 860  
 781 CTAAAGCATGCACTAGTGTGGGCTTATTAAGGCTTG--GTAAAGAGCTTAAAGCGGT 838  
 861 GTAAAGCATGCACTAGTGTGGGCTTATTAAGGCTTG--GTAAAGAGCTTAAAGCGGT 920  
 839 GAATTTGACCGGCTGGGAGAGTACGCTGCAAGATTAATCAACAGAGATTAAGAGGAGAC 898  
 921 TAAATATTCGCGCTGGGAGAGTACGCTGCAAGATTAATCAACAGAGATTAAGAGGAGAC 980  
 899 CCGCAGACAGCGGTGATTAATGATTAATTCATGACAGCGAGAAACCTTACCTAACCC 958  
 981 CCGCAGACAGCGGTGATTAATGATTAATTCATGACAGAGAAACCTTACCTAACCGGC 1040

Qy 959 TTGACATGAGCGCAATTTTCTAGAGATAGTATGTC-CTTGGGAGCGTTACAGAGTG 1017  
 Db 1041 TTGACATGAGCGCAATTTTCTAGAGATAGTATGTC-CTTGGGAGCGTTACAGAGTG 1100  
 Qy 1018 CTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1077  
 Db 1101 GTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1160  
 Qy 1078 ACCCTGCTATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1137  
 Db 1161 ACCCTGCTATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1219  
 Qy 1138 CCGAG 1197  
 Db 1220 CCGAG 1279  
 Qy 1198 TAAATACATGAGCGCTGACAGAGGCTTCCAAACCGCGAGGAGGAGCTTAATCTCAAG 1257  
 Db 1280 TGCTACATGAGCGCTGACAGAGGCTTCCAAACCGCGAGGAGGAGCTTAATCTCAAG 1339  
 Qy 1258 GCGTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1317  
 Db 1340 GCTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1399  
 Qy 1318 GCGGATCAG-CATGTCGCGGCTGATTAATGCTTCCGCGGCTTGTACACACCGCGCTCA 1376  
 Db 1400 GCGGATCAG-CATGTCGCGGCTGATTAATGCTTCCGCGGCTTGTACACACCGCGCTCA 1459  
 Qy 1377 CCATGAGAGTGGGCTTCCACAGAGCAGAGTATGTC-TAACCTTAAGAGAGGAGCTTGCAC 1435  
 Db 1460 CTATAGAGCTGCGCATGTTGAAGTCAATCACTTAACCTTAAGAGAGGAGGAGGAGCTTAA 1519  
 Qy 1436 GTGAGATTCATGACTGCGGTG 1457  
 Db 1520 GCGTACGCTTGCAGCTGAGTG 1541

## RESULT 3

BH814966/c 1143 bp DNA linear GSS 31-MAY-2003  
 LOCUS  
 DEFINITION  
 bpPC15, Maize B chromosome PCR DNA library Zea mays genomic clone  
 BH814966  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

Zea mays  
 Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoidae; Andropogoneae; Zea.

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 PUBMED  
 COMMENT

1 (bases 1 to 1143)  
 Cheng, Y.M. and Lin, B.Y.  
 Cloning and characterization of maize B chromosome sequences  
 derived from microdissection  
 Genetics 164 (1), 299-310 (2003)  
 12750341  
 Contact: Bor-yaw Lin  
 Department of Molecular Biology  
 National Chung Hsing University  
 250 Kuo Kuang Rd, Taichung 402, Taiwan (ROC)  
 Tel: 886-4-2285-1885  
 Fax: 886-4-2287-4879  
 Email: bylin@dragon.nchu.edu.tw  
 Insert Length: 1143 Std Error: 0.00  
 Class: PCR fragment.

## FEATURES

source  
 1. 1143  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /cultiivar="L289"  
 /db\_xref="taxon:4577"  
 /clone="bpPC15"

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/sex="thermaphrodite"
/cell_type="pollen mother cells"
/dev_stage="Meiosis I"
/lab_host="DHSalpha"
/clone_lib="Maize B chromosome PCR DNA library"
/notes="Vector: pBSK-; The library was constructed from
microdissected B chromosome DNA."

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ORIGIN
Query Match      44.5%; Score 648.4; DB 9; Length 1143;
Best Local Similarity 89.6%; Pred. No. 9,9e-189;
Matches 744; Conservative 0; Mismatches 76; Indels 10; Gaps 4;

QY 631 CAGAGGAGGTGTAATTCATGCTGAGTGAATTCGATGATGGAAGAACTCG 630
DB 1143 CAGAGGAGGTGTAATTCATGCTGAGTGAATTCGATGATGGAAGAACTCG 1084
QY 691 ATGGCGAAGGACAGCTCTGGGTTAACTGACGCTCATGACAGAAAGCGTGGGAGCAA 750
DB 1083 ATGGCGAAGGACAGCTCTGGGTTAACTGACGCTCATGACAGAAAGCGTGGGAGCAA 1024
QY 751 ACAGATTAGATACCTGTAAGTCCAGCCCTTAACGATGCACTAGTTGGGCTT 810
DB 1023 ACAGATTAGATACCTGTAAGTCCAGCCCTTAACGATGCACTAGTTGGGCTT 964
QY 811 ATTAGCTTGTATACCAAGCTTAACGCTGAAGTTGAACGCTGGGAGTACGGTCCAG 870
DB 963 AATTGACGTTGTATACCAAGCTTAACGCTGAAGTTGAACGCTGGGAGTACGGTCCAG 904
QY 871 ATTAAGCTCAAGAAATTAACGGGAGCCGCAACAGCGGTGATTAATGATTAATTC 930
DB 903 ATTAAGCTCAAGAAATTAACGGGAGCCGCAACAGCGGTGATTAATGATTAATTC 844
QY 931 GATGCAACGGGAAATCTTACCTACCTTGAACATGTAAGCAATTTCTAGATAGATT 990
DB 843 GATGCAACGGGAAATCTTACCTACCTTGAACATGTAAGCAATTTCTAGATAGATT 784
QY 991 AGTGCT---TCGGGAAAGCTTAACAGAGTGTGATGCTGCTGCTGCTGCTGCTGA 1047
DB 783 AGTGCTGAAGAAAGCACTGATACAGAGTGTGATGCTGCTGCTGCTGCTGCTGA 724
QY 1048 GATGTTGGTGAAGTCCCGCAACAGCGCAACCTTGTCAATTAATGCTCAATTTGGTT 1107
DB 723 GATGTT--GTTAAGTCCCGCAACAGCGCAACCTTGTCAATTAATGCTCAATTTGGTT 670
QY 1108 GGGCACTTAATAGACTGCGGTGACAAACCGAGAGAGTGGGATGACGTCAAGTCC 1167
DB 669 GGGCACTTAATAGACTGCGGTGACAAACCGAGAGAGTGGGATGACGTCAAGTCC 611
QY 1168 TCATGGCCCTTAATGAGGAGCTTCAACAGTAATTAACAATGGCGCTACAGAGGTTGCCA 1227
DB 610 TCATGGCCCTTAATGAGGAGCTTCAACAGTAATTAACAATGGCGCTACAGAGGTTGCCA 551
QY 1228 ACCCGGAGGAGGAGTAATCTCAAGAAAGCGCTGTAAGTCCGATCGAGTCTGCAACT 1287
DB 550 ACCCGGAGGAGGAGTAATCTCAAGAAAGCGCTGTAAGTCCGATCGAGTCTGCAACT 491
QY 1288 CGATCCGTAAGTCCGATCGTAAGTATGCGGATCAAGATGTCGGGTGAATACGTT 1347
DB 490 CGATCCGTAAGTCCGATCGTAAGTATGCGGATCAAGATGTCGGGTGAATACGTT 431
QY 1348 CCGGGGCTTGTACACACCGCGCTCACACATGGGAGTGGGTTTCCAGAGAGCGGTA 1407
DB 430 CCGGGGCTTGTACACACCGCGCTCACACATGGGAGTGGGTTTCCAGAGAGCGGTA 371
QY 1408 GTCTAAACCTTAAGAGAGGCGCTTGCCACGCTGAAGATTCATGACTGGGGT 1457
DB 370 GTCTAAACCTTAAGAGAGGCGCTTGCCACGCTGAAGATTCATGACTGGGGT 321

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RESULT 4
B2439740      1084 bp      DNA      linear      GSS 13-DEC-2002
LOCUS      B2439740

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DEFINITION      BONDUS4TF BO.1.6.2 KB tot Brassica oleracea genomic clone BONDUS4,
genomic survey sequence.
ACCESSION      B2439740
VERSION      B2439740.1 GI:26695676
KEYWORDS      GSS.
SOURCE      Brassica oleracea
ORGANISM      Brassica oleracea

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```

REFERENCE      1 (bases 1 to 1084)
AUTHORS      Ayele,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S.,
Utecherback,T.R., Wortman,J.R., White,O.R. and Town,C.D.

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TITLE      Whole genome shotgun sequencing of Brassica oleracea and its
JOURNAL      application to gene discovery and annotation in Arabidopsis
PUBMED      genome Res. 15 (4), 487-495 (2005)
COMMENT      15805490
Other GSSs: BONDUS4TF
CONTACT: Chris Town
TIGR

```

```

9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: sheared ends.

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FEATURES
Source
Location/Qualifiers
1..1084
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone_lib="BONDUS4"
/notes="Vector: PHOS1; Site 1: BstXI, 1.6-2 kb sheared
total DNA inserted into PHOS1 using BstXI linkers"

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## ORIGIN

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Query Match      44.0%; Score 641.4; DB 9; Length 1084;
Best Local Similarity 77.2%; Pred. No. 1,4e-186;
Matches 841; Conservative 0; Mismatches 221; Indels 27; Gaps 4;

QY 237 CTACCAAGCGAGTCACTAGTGTGATGAGAGGACCAAGCACTGGAGTGA 296
DB 3 CTACCAAGCGAGTCACTAGTGTGATGAGAGGACCAAGCACTGGAGTGA 61
QY 297 CACGGCCAGACTCTACCGGAGGACAGTGGGAAATTTGCAATGAGGCGCAAGCT 356
DB 62 CACGGCCAGACTCTACCGGAGGACAGTGGGAAATTTGCGCAATGAGGCGCAAGCT 121
QY 357 GATCCAGCAATGCGCGGTGATGAGAGAGCCCTCGGGTTGAAAGCTCTTTCAAGTCGAG 416
DB 122 GAGCGGCAATGCGCGGTGATGAGAGAGCCCTACCGGTCCTGAACCTTTTCCAGAG 181
QY 417 AAGAAAGGTTACGTAATTAATCGTCACTGACGATGATGCAAGAGAGACACCGGC 476
DB 182 AAGA-----ACCAATGACGATCTGGGAAATAGCATTCGCGC 218
QY 477 TAACAGTGCAGACAGCCGCGTAATTAAGAGGTGCAAGCGTTAATCGAATTA 536
DB 219 TAACAGTGCAGACAGCCGCGTAATTAAGAGAGTCAAGCGTTAATCGAATTA 278
QY 537 GCGTAAAGGTCGCGAGGCGGCTTTGATGATGATGTAATTCGCCGGGCTTAACCTG 596
DB 279 GCGTAAAGGTCGTAAGTGTGCTTTTAAGTCCGCGTAATTCAGAGGCTCAACCTG 338
QY 597 GAATTCGTTTGAATCAAGAGTGAAGTGGACAGAGGAGTGAATTCATGATGA 656
DB 339 GACAGCGGTGAAATTAACAGCTTGATGAGTGGGCGAGAGGAATTTCCGGTGA 398
QY 657 GCAGTGAATGCGTGAATGAGAAAGATGATGCGGAAGGACGCTCTGGGTTAA 716

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Db      399 GCGGTGAAGATCGTAGAGATCGGAAAGAACCAACGCGGAAAGACCTCTGCTGGCCGA 458
Qy      717 CACTGACGCTCATGACGAAAGCTGGGAGCAACAGGATTAGTACCTGTGTATGCTCA 776
Db      459 CACTGACACTGAGAGACGAAAGCTGAGGAGCGAATGAGATTAGTACCCCGAGTGTCT 518
Qy      777 GCGCCTAAAGATGCACTAGTGTGTTGGGCTTTATTTAGGCTTG--GTAGCAAGACTTAC 834
Db      519 AGCCGTAAACGATGATCTAGGCGCTGTGCTATGACCCGCTGAGCTGTACTTAC 578
Qy      835 GCGTGAAGTTGACCGCTGGGAGTACCGTGCAGATTTAAACTCAAGAGATTGACG 894
Db      579 GCGTTAAGTATCCGCTCGGGAGTACGTTGCGAAGATGAAGAACTCAAGAGATTGACG 638
Qy      895 GGACCCGCAAGACCGGTGATTTATGATTTATGATGCAACCGGAAAACTTACTT 954
Db      639 GGGCCCGCAAGCGGTGAGCATGTGTTTATTCATGCAAGCAAGAACTTACCA 698
Qy      955 ACCCTGACATGACGGAATTTCTAGAGATGATTAATG--CTTGGGAGGCTTACCA 1013
Db      699 GGGCTGACATGCGCGGATCTCTTGAAGAGAGGGGTGCTTGGGAAACGCGACCA 758
Qy      1014 GGTGCTGATGAGCTGTCTGAGCTGTGCTGATGATGTTGGTTAAGTCCGCAACGAG 1073
Db      759 GGTGCTGATGAGCTGTCTGAGCTGTGCTGATGATGTTGGTTAAGTCCGCAACGAG 818
Qy      1074 CGCAACCTTGTCTATTATTTGCTCATTTGTTGGTGGCACTTTAATGAGCTGCGGTGA 1133
Db      819 CGCAACCTTGTCTATTATTTGCTCATTTGTTGGTGGCACTTTAATGAGCTGCGGTGA 878
Qy      1134 CAACCCGAGAGAGGTGGGAGTGAAGTCAAGTCCCTCAAGGCTTATGAGGCTTCA 1193
Db      879 TAAAGCGAGAGAGGTGGGAGTGAAGTCAAGTCAAGTCCCTTATGCTGAGGCTCA 938
Qy      1194 CACGTAATACATGCGCGCTGACAGAGGTTGCCAACCGCGAGGGAGCTAATCTCAGA 1253
Db      939 CACGTCATACATGCGCGGAGCAAGGTCGAGTCCGCGAGGGTGAAGCTTACCTCAAA 998
Qy      1254 AAGGCGCTGATGTCGAGTGGAGTCTGCACTGCACTCGTGAAGTGGATGCTAG 1313
Db      999 AACCCTGCTCAGTGGATGTCAGGCTGCACTCGCTGATGAAGCGGATGCTAG 1058
Qy      1314 TAATCGCGG 1322
Db      1059 TAATCGCGG 1067

RESULT 5
LOCUS   CK296497 941 bp mRNA linear EST 02-AUG-2004
DEFINITION EST759211 Nicotiana benthamiana mixed tissue cDNA library,
normalised, full-length Nicotiana benthamiana cDNA clone NEMD226 5'
end, mRNA sequence.
ACCESSION CK296497
VERSION   CK296497
KEYWORDS EST.
SOURCE   Nicotiana benthamiana
ORGANISM Nicotiana benthamiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiales; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 941)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
Stebkiewicz, B., Jin, H. and Baker, B.
Generation of EST sequences from Nicotiana benthamiana
Unpublished (2003)
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@igf.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
Seq primer: ATT TAG GTG ACA CTA TAG.

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FEATURES
Source
Location/Qualifiers
1..941
/organism="Nicotiana benthamiana"
/mol_type="mRNA"
/db_xref="taxon:4100"
/clone="NEMD226"
/tissue_type="abiotic and biotic stress-treated leaves,
callus tissue and root tissue"
/lab_host="DH10B-TonA"
/clone_id="Nicotiana benthamiana mixed tissue cDNA
library, normalised, full-length"
/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: RNA was isolated from Nicotiana benthamiana
tissues that include callus, roots from liquid culture
grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
challenged leaves (Pseudomonas syringae pv tomato 12 hr;
Xanthomonas syringae pv campestris 12 hr, 18hr;
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
amounts."

ORIGIN
Query Match 43.8%; Score 637.8; DB 7; Length 941;
Best Local Similarity 81.3%; Pred. No. 1,86-185;
Matches 752; Conservative 0; Mismatches 172; Indels 1; Gaps 1;

1 ATTGAACGCTGGCGGCGATGCTTTACACATGCAAGTCGACGCGACGATGCTTGAT 60
18 ATTGAACGCTGGCGGCGGCGGCTTTACACATGCAAGTCGACGCGGCGGCGGCTTGTAC 77
61 CTGTGCGGAGTGGCGGAGCGGTGATGATGATGATGATGATGATGATGATGATGATGAT 120
78 CTGTGCGGAGCGGCGGAGCGGTGATGATGATGATGATGATGATGATGATGATGATGAT 137
121 ACGCATGAAAGATGCTCTAATACCGCATATCTCTAAGAGAGAAACGAGGAGATGCAAA 180
138 ACGCTCGAAACGAGACGCTAATACCGCATATCTCTAAGAGAGAAACGAGGAGATGCA 197
181 GACCTTGGCTTTTGAAGCGGCGGATGCTGATGATGATGATGATGATGATGATGATGATG 240
198 GACCTTGGCTTTTGAAGCGGCGGATGCTGATGATGATGATGATGATGATGATGATGATG 257
241 CAAGCGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 300
258 CAAGCGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 317
301 GCCGAGCTCCTTACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 360
318 GTCCAGACTCTTACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 377
361 CAGCAATGCCCGCTGATGAGAGAGGCTTGGGTTGTAAGCTCTTCACTGAGAGAGA 420
378 CAGCAATGCCCGCTGATGAGAGAGGCTTGGGTTGTAAGCTCTTCACTGAGAGAGA 437
421 AAGGTTAAGGTTAATATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 480
438 AAGGTTAAGGTTAATATGCTGATGATGATGATGATGATGATGATGATGATGATGATG 497
481 TAGTGGCAGAGCGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540
498 TGTGTCAGAGAGCGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 557
541 AAGGTTGCGAGCGGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 600
558 AAGGCGGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 617
601 TGGCTTGAATCAATCAAGGTTAGTGTGATGATGATGATGATGATGATGATGATGATGATG 660
618 TGCAATCAAAATCGGCAAGCTAGAGTGTGATGATGATGATGATGATGATGATGATGATG 677
661 TGAATCGTAGATATGAGAGACATGATGCGAAGGCGGCTCTGAGTTAAGACT 720

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Db      678 TGAATGCGTAGATATGAGAAACACAGTGGCCAGAGCCACTGATGATCT 737
Qy      721 GAGCTCATGACGAAAGCGTGGGAGCAAAAGATTAGATACCTGTATGCCAGCC 780
Db      738 GACATGAGGTGGAAAGCGTGGGAGCAAAAGATTAGATACCTGTATGCCAGCC 797
Qy      781 CTAAAGATGTCATCTAGTGTGTTGGGCTTATAGGCTTGTAACGAACTAACGCTGA 840
Db      798 GTAAAGATGTCATCTAGTGTGTTGGG-AGCCTTAGAGCTTATAGTGGCACTAACGCAATTA 856
Qy      841 AGTTGACCGGCTGGGAGTACGGTCCGCAATTAACCTCAAGAAATTGACGGGAGCC 900
Db      857 AGTTGACCGGCTGGGAGTACGGTCCGCAATTAACCTCAAGAAATTGACGGGAGCC 916
Qy      901 GCACAAAGCGGTGATTAATGATGATT 925
Db      917 GCACAAAGCGGTGATTAATGATGATT 941

```

RESULT 6  
B2447500/c 1053 bp DNA linear GSS 13-DEC-2002  
LOCUS BONKF40TR BO.1.6.2 KB tot Brassica oleracea genomic clone BONKF40,  
DEFINITION genomic survey sequence.

ACCESSION B2447500  
VERSION B2447500.1 GI:26712943  
KEYWORDS GSS.  
SOURCE Brassica oleracea  
ORGANISM Brassica oleracea

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
Rosids; eustoids II; Brassicales; Brassicaceae; Brassica.

Ayale, M., Haas, B.J., Kumar, N., Wu, H., Xiao, Y., Van Aken, S.,  
Utecherback, T.R., Wortman, J.R., White, O.R. and Town, C.D.  
Whole genome shotgun sequencing of Brassica oleracea and its  
application to gene discovery and annotation in Arabidopsis  
Genome Res. 15 (4), 467-495 (2005)

JOURNAL PUBMED  
COMMENT Other GSSs: BONKF40TF  
Contact: Chris Town

TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA.  
Tel: 301-838-3523  
Fax: 301-838-0208  
Email: cdtown@tigr.org  
DNA is from a doubled haploid provided by Tom Osborn.  
Seq primer: TR  
Class: sheared ends.

FEATURES  
source Location/Qualifiers

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/mol\_type="genomic DNA"  
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/clone="BONKF40"  
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total DNA inserted into pHD51 using BstXI linkers"

ORIGIN

Query Match 43.5%; Score 633.2; DB 9; Length 1053;  
Best Local Similarity 77.2%; Pred. No. 4,9e-184;  
Matches 831; Conservative 0; Mismatches 218; Indels 27; Gaps 4;

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Db      1052 GGCTCCCGCTGATGCTAGTGTGGGTAAAGGCTTCAAGAGGAGCATGATG 259
Qy      260 TGGTGTGAAGAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 319
Db      992 TGGTGTGAAGAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 319

```

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Qy      320 GGAGAGTGGGGAATTTTGGACATGGGGCAAGGCTGATCCAGCAATGCGCGTAGTG 379
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Qy      380 AAGAAAGCCTTCGGGTGTTAAAGCTCTTCACTGAGAGAAAGAAAGTTACGGTAAATAT 439
Db      873 TAGAAGCCTTACGGGTCTGAACTTTTCCCAAGAAAG----- 833
Qy      440 CGTGAAGTCAAGCGGTATGACAGAAAGACACCGGCTTACTAGTCCAGACCGCGG 499
Db      832 ----AGCAATGACGGTATCTGGGGAATTAAGCATCCGCTTAACCTGTGCGACGACGCGG 777
Qy      500 TAATAGTGAAGGTGGAAGGTTAATCCGAAATTAAGGCGGTAAAGGTGCGAGCGGCT 559
Db      776 TAATAGTGAAGGTGGAAGGTTAATCCGAAATTAAGGCGGTAAAGGTGCGAGCGGCT 717
Qy      560 TTGTAAAGTCAAGTGAATATCCCGGCTTAACTGGAATTCGTTGAAACTACAAAG 619
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Qy      1217 GAGGGTTCACCAACCGGAGAGGAGGAGTAACTCTCAAGAAAGGCGGTGAGTCCGGA 1272
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RESULT 7  
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DEFINITION genomic survey sequence.  
ACCESSION B2431523  
VERSION B2431523.1 GI:2677909

KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
PUBMED  
COMMENT

GSS  
Brassica oleracea  
Brassica oleracea  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
1 (bases 1 to 1010)  
Ayele,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S., Uteirack,T.R., Wortman,J.R., White,O.R. and Town,C.D.  
Whole genome shotgun sequencing of Brassica oleracea and its application to gene discovery and annotation in Arabidopsis  
Genome Res. 15 (4), 487-495 (2005)  
15805490  
Other GSSs: BOMND88TR  
Contact: Chris Town  
TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA.  
Tel: 301-838-3523  
Fax: 301-838-0208  
Email: cdtown@tigr.org  
DNA is from a doubled haploid provided by Tom Osborn.  
Seq primer: TF  
Class: sheared ends.

FEATURES  
source  
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Location/Qualifiers  
/organism="Brassica oleracea"  
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ORIGIN  
Query Match 43.1%; Score 627.8; DB 9; Length 1010;  
Best Local Similarity 77.9%; Pred. No. 2,3e-182;  
Matches 805; Conservative 0; Mismatches 202; Indels 26; Gaps 3;

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890 GAATTTTCCGAAATGGGGCGAAGCCTGATCCAGCAATGCCGGGTGAGTGAAGAGCCCTT 831  
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830 CGGGTCCGAACTCTTCCCAAGAGAGA-----AGCAATG 794  
451 ACGGATTCGACAAAGAGACACCGGCTAATCACTGCGCAGACGCGCGGTAAATAGTAG 510  
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RESULT 8  
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LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

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genomic survey sequence.  
BH705272  
BH705272.1 GI:18787746  
GSS.  
Brassica oleracea  
Brassica oleracea  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
1 (bases 1 to 1079)  
Ayele,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S., Uteirack,T.R., Wortman,J.R., White,O.R. and Town,C.D.  
Whole genome shotgun sequencing of Brassica oleracea and its application to gene discovery and annotation in Arabidopsis  
Genome Res. 15 (4), 487-495 (2005)  
15805490  
Other GSSs: BOMKA47TR  
Contact: Chris Town  
TIGR  
9712 Medical Center Drive, Rockville, MD 20850, USA.  
Tel: 301-838-3523  
Fax: 301-838-0208  
Email: cdtown@tigr.org  
DNA is from a doubled haploid provided by Tom Osborn.  
Seq primer: TF  
Class: sheared ends.

FEATURES  
source  
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Location/Qualifiers  
/organism="Brassica oleracea"  
/mol\_type="genomic DNA"



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 QY 560 TTGTAATGATGATGTAATCCCGGCTTAACCTGCGAATTCGTTGAAACTACAGG 619  
 DB 679 TTTTAATGTCGGCGTCAATCCAGGGGCTCAACCTCGGACAGCGGCTGAAACTCAAG 620  
 QY 620 CTAGATGTCGAGAGGAGGAGGATTCAGATGATGAGAGAAATGGTGAAGATG 679  
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 QY 680 GAAGAACATCGATGCGAGGAGCGCTCTCGGCTTAACATGACGCTCATGACGAAAGC 739  
 DB 559 AAAGAACACCAACGCGGAAAGCACTGCTGGGCGGACATGACATGAGAGACGAAAGC 500  
 QY 740 GTGGGAGACAAACAGATTAATGATACCTGCTGATCCAGCCCTAAACGATGCAACT 799  
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 ACCESSION BH656222  
 VERSION BH656222.1 GI:18714532  
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 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
 REFERENCE 1 (bases 1 to 1031)  
 AUTHORS Ayale, M., Haas, B.J., Kumar, N., Wu, H., Xiao, Y., Van Aken, S.,

TITLE Utterback, T.R., Wortman, J.R., White, O.R. and Town, C.D.  
 JOURNAL Whole genome shotgun sequencing of Brassica oleracea and its  
 PUBMED application to gene discovery and annotation in Arabidopsis  
 COMMENT Genome Res. 15 (4), 487-495 (2005)  
 15805490  
 CONTACT: Chris Town  
 TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA.  
 Tel: 301-838-3523  
 Fax: 301-838-0208  
 Email: cdtown@tigr.org  
 DNA is from a doubled haploid provided by Tom Osborn.  
 Seq primer: TP  
 Class: sheared ends.

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 genomic DNA inserted into pHD01 using BstXI linkers"

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 Query Match 42.4%; Score 617.4; DB: 9; Length 1031;  
 Best Local Similarity 76.5%; Pred. No. 3.8e-119;  
 Matches 806; Conservative 0; Mismatches 221; Indels 26; Gaps 3;

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 QY 367 TCCGCGTGAATGAGAAAGCCTTGGGCTGTAAAGCTCTTTCAGTGCAGAAAGAACT 426  
 DB 971 TCCGCGTGAATGAGAAAGCCTTGGGCTGTAAAGCTCTTTCAGTGCAGAAAGAACT 918  
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 DB 917 -----AGCAATGACGATCTGCGGAAATTAAGATGATGATGATGATGATGATG 875  
 QY 487 CCAGCAGCGCGGTAATTAAGTGTGCAACGCTTAATCGGAATTAATGATGATGATGATG 546  
 DB 874 CCAGCAGCGCGGTAATTAAGTGTGCAACGCTTAATCGGAATTAATGATGATGATG 815  
 QY 547 TCCGAGGCGGCTTGTAACTGATGATGATGATGATGATGATGATGATGATGATG 606  
 DB 814 TCTGTAGGTGCTTTTAATGCTCCGCTCAAAATCCAGAGGCTCAACCTGACAGCGGT 755  
 QY 607 TGAATCTAAGGCTTAAGTGTGCAAGAGAGTGAATTCATGATGATGATGATGATG 666  
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 DB 274 GTGTTTAGTTGCCACCGTTGAGTTGAAACCTGAACAGATCGCGGTGATTAAGCCGAG 215  
 QY 1144 GAAGGTGGGAGATAGCTGCAAGTCTCATGCGCTTATGGGAGGCTTCACAGTAAATAC 1203  
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RESULT 11  
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 VERSION BZ450751.1 GI:26721334  
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SOURCE Brassica oleracea  
 ORGANISM Brassica oleracea  
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 1077)  
 Ayala, M., Haas, B.J., Kumar, N., Wu, H., Xiao, Y., Van Aken, S.,  
 Utechtack, T.R., Wortman, J.R., White, O.R. and Town, C.D.  
 Whole genome shotgun sequencing of Brassica oleracea and its  
 application to gene discovery and annotation in Arabidopsis  
 Genome Res. 15 (4), 487-495 (2005)  
 JOURNAL PUBMED 15805490  
 COMMENT Other\_GSSs: BOMB063TR  
 Contact: Chris Town

TIGR  
 9112 Medical Center Drive, Rockville, MD 20850, USA.  
 Tel: 301-838-3523  
 Fax: 301-838-0208  
 Email: cdtown@tigr.org  
 DNA is from a doubled haploid provided by Tom Osborn.  
 Seq primer: TR  
 Class: sheared ends.

FEATURES  
 source location/Qualifiers

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 total DNA inserted into pHD51 using BclXI linkers"

ORIGIN  
 Query Match 42.2%; Score 615.2; DB 9; Length 1077;

Best Local Similarity 77.5%; Pred. No. 1,9e-178;  
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 DB 128 AGGATCAAGCGTAAATCGGAATTAATCTAGGCGTAAAGCGTGTAGTGTCTTTTAACT 187  
 QY 568 CAGATGGAATCCCGGCTTAACCTGGGAAATGCGTTGAAACTAACAAGGCTAGAGTG 627  
 DB 188 CCGCGCTCAATCCAGGGCTCAACCTGGAACAGGGGTGGAACCTAACAGGCTTAGTA 247  
 QY 628 TGGCAGAGGAGTGAATTCATGTGTAGCAAGTAAATGCGTAAATGAGATAGAAACA 687  
 DB 248 CGGTAGGGGAGAGGGAATTTCCGTTGAGCGGTGAATGCGTAAAGATCGAAAGACA 307  
 QY 688 TCGATGGCGAAGGCAAGCTCTCTGGGTTAACTGACGCTCATGACGAAAGCGTGGGAG 747  
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 QY 748 CAAACAGATTAGATACCTGTAGTCAAGCCCTAAAGATGCACTAGTTGGGC 807  
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 QY 926 AATTGATGCAAGCGGAAACCTTACTCACTTGTGATGATGCAATTTTCTAGAT 985  
 DB 548 AATTGATGCAAGCGGAAACCTTACTCACTTGTGATGATGCAATTTTCTAGAT 607  
 QY 986 AGATTAGTG-CTTCGGGAAACGCTAACACAGGTGCTGATGCTGTGCTGCTGTGCTG 1044  
 DB 608 AGAGGGGTGCTTCGGGAAACGCGGACAGGTGTGCTAGTGTGCTGTGCTGTGCTG 667  
 QY 1045 TGAATGTTGGGTTAGTCCCGGCAAGAGGCAACCTGTCTTAATTGCAATTTG 1104  
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 ORGANISM Brassica oleracea  
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 Ayale, M., Haas, B.J., Kumar, N., Wu, H., Xiao, Y., Van Aken, S.,  
 Utebäck, T.R., Wortman, J.R., White, O.R. and Town, C.D.  
 Whole genome shotgun sequencing of Brassica oleracea and its  
 application to gene discovery and annotation in Arabidopsis  
 JOURNAL Genome Res. 15 (4), 487-495 (2005)  
 PUBMED 15805490  
 COMMENT Other GSSs: BOMK86TR  
 Contact: Chris Town  
 TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA.  
 Tel: 301-838-3523  
 Fax: 301-838-0208  
 Email: cdtown@tigr.org  
 DNA is from a doubled haploid provided by Tom Osborn.  
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 1 (bases 1 to 1051)  
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 Utebäck, T.R., Wortman, J.R., White, O.R. and Town, C.D.  
 Whole genome shotgun sequencing of Brassica oleracea and its  
 application to gene discovery and annotation in Arabidopsis  
 JOURNAL Genome Res. 15 (4), 487-495 (2005)  
 PUBMED 15805490  
 COMMENT Other GSSs: BOMHR54TR  
 Contact: Chris Town  
 TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA.  
 Tel: 301-838-3523  
 Fax: 301-838-0208  
 Email: cdtown@tigr.org  
 DNA is from a doubled haploid provided by Tom Osborn.  
 Seq primer: TR  
 Class: sheared ends.  
 Location/Qualifiers  
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Best Local Similarity 78.5%; Pred. No. 7.6e-178;
Matches 772; Conservative 0; Mismatches 208; Indels 4; Gaps 3;

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QY 1225 CCAACCGGAGGGGAGGCTAATCTCAGAAAGCGCGTATGTCGGATCGGAGTGTGCA 1284
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VERSION CK280527
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1 (bases 1 to 889)
REFERENCE Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
Staskiewicz, B., Jia, H. and Baker, B.,
Generation of EST sequences from Nicotiana benthamiana
Unpublished (2003)
Other ESTs: ESR743250
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-aray@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
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challenged leaves (Pseudomonas syringae pv tomato 12 hr;
Xanthomonas campestris pv campestris 12 hr, 18hr;
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
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challenged leaves (Pseudomonas syringae pv tomato 12 hr;
Xanthomonas campestris pv campestris 12 hr, 18hr;
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from
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amounts."

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RESULT 15      884 bp      mRNA      linear      EST 02-AUG-2004
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LOCUS          normalized, full-length Nicotiana benthamiana cDNA clone NBMA117 5'
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VERSION        CK280528.1 GI:39850200
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ORGANISM       Nicotiana benthamiana
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 884)
Buell, C.R., Hart, A., Ziemann, V., Karimychewa, S.A., Day, B.,
Staskiewicz, B., Jin, H. and Baker, B.
Generation of EST sequences from Nicotiana benthamiana
JOURNAL
COMMENT        Unpublished (2003)
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      cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
      challenged leaves (Pseudomonas syringae pv tomato 12 hr;
      Xanthomonas campestris pv campestris 12 hr, 18hr;
      Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
      campestris pv vesicatoria 18hr). RNA was isolated from
      these tissues and pooled in approximately equal molar
      amounts."

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## ORIGIN

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Oy 121 ACGCATCGAAGATGCTAATACCGCATATATCTTAAGAGAGAAAGCAGGGATCGA 180
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Contact: Robin Buell  
The Institute for Genomic Research  
9712 Medical Center Dr, Rockville, MD 20850, USA  
Email: potato-array@igr.org  
Clones can be requested from the University of Arizona Genomics  
Institute via <http://genome.arizona.edu/orders/>.  
Seq primer: CAG GAA ACA GCT ATG ACC.

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| 9  | 1287.6 | 88.4  | 1458  | 12   | ADM32706  | Adm32706  | AOB Type  |
| 10 | 1230.2 | 84.4  | 1460  | 6    | ABA02419  | AbA02419  | Type C am |
| 11 | 1230.2 | 84.4  | 1460  | 12   | ADM32707  | Adm32707  | AOB Type  |
| 12 | 1206.4 | 82.8  | 1485  | 4    | AAC866030 | Aac866030 | 16s rDNA, |
| 13 | 1197.2 | 82.2  | 1495  | 6    | AB078660  | Ab078660  | Nucleotid |
| 14 | 1194   | 81.9  | 1460  | 4    | AAC866026 | Aac866026 | 16s rDNA, |
| 15 | 1190.8 | 81.7  | 1464  | 6    | AB140355  | Ab140355  | Sequence  |
| 16 | 1181   | 81.1  | 1459  | 4    | AAC866028 | Aac866028 | 16s rDNA, |
| 17 | 1179.2 | 80.9  | 1460  | 4    | AAC866024 | Aac866024 | R. tenuis |
| 18 | 1161   | 79.7  | 1530  | 13   | ADR44500  | Adr44500  | 16S rRNA  |
| 19 | 1156.8 | 79.4  | 1460  | 4    | AAC866022 | Aac866022 | R. tenuis |

New bacteria capable of oxidizing ammonia to nitrite, for preventing or alleviating the accumulation of ammonia in fresh water aquaria, seawater aquaria and waste water.

Claim 2; Page 5; 62pp; English.

The invention relates to 4 novel types of ammonia-oxidising bacteria (AOB) found in freshwater aquaria. The bacteria are able to oxidise ammonia to nitrite and are members of the ammonia-oxidising bacteria family of the beta subdivision of Proteobacteria. The 4 types of bacteria can be distinguished on the basis of their 16S rRNA (ribosomal RNA) gene

CC sequences (ABA02416-ABA02419), and are classified as AOB type A (e.g., R7clone140), type A1 (e.g., R7clone187), type B (e.g., R3clone5) and type C (e.g., R3clone47). The invention also encompasses isolated 16S rRNA gene sequences of the ammonia-oxidising bacteria of the invention, CC oligonucleotide probes and primers for the detection of these bacteria, CC and compositions comprising the bacteria. The bacteria of the invention are useful in biological filters for reducing ammonia accumulation in CC both freshwater and seawater aquaria. They may also be used in waste CC water treatment and in bioremediation processes to reduce the level of CC pollution caused by ammonia. The present sequence represents R7clone140, CC a 16S rRNA gene sequence from the type A ammonia-oxidising bacterium of CC the invention. (Updated on 29-AUG-2003 to standardise OS field)

XX Sequence 1457 BP; 378 A; 315 C; 456 G; 308 T; 0 U; 0 Other;

Query Match 100.0%; Score 1457; DB 6; Length 1457;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1457; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTGAACGCTGGCGGCATGCTTTACATGCAAGTCAAGCGGAGCAACGCGATCTTGCAT 60  
 DB 1 ATTGAACGCTGGCGGCATGCTTTACATGCAAGTCAAGCGGAGCAACGCGATCTTGCAT 60

QY 61 CTGGTGGCGAGTGGCGGAGCGGTGAGTAAATGATCGGACGATCCAGAGAGGGGGTA 120  
 DB 61 CTGGTGGCGAGTGGCGGAGCGGGTGAATGATCGGACGATCCAGAGAGGGGGTA 120

QY 121 ACGCATCGAAGATGTGCTAAATACCCCATATATCTTAAGGAGAAAGACGAGGGGATCGAAA 180  
 DB 121 ACGCATCGAAGATGTGCTAAATACCCCATATATCTTAAGGAGAAAGACGAGGGGATCGAAA 180

QY 181 GACCTTGGCGCTTTGAGGCGCGCATGCTGATAGCTAGTGTGGGTAAAGGCTTAC 240  
 DB 181 GACCTTGGCGCTTTGAGGCGCGCATGCTGATAGCTAGTGTGGGTAAAGGCTTAC 240

QY 241 CAAGGCGAGTCACTAGTGTGGTCTGAGAGGAGCGACCCACACTGGGACCTGAGACAG 300  
 DB 241 CAAGGCGAGTCACTAGTGTGGTCTGAGAGGAGCGACCCACACTGGGACCTGAGACAG 300

QY 301 GCCCAGACTCTTACGGGAGCGCAGTGGGGATTTGGACAAATGGGCGCCAGCCCTGATC 360  
 DB 301 GCCCAGACTCTTACGGGAGCGCAGTGGGGATTTGGACAAATGGGCGCCAGCCCTGATC 360

QY 361 CAGCAATGCGCGTGAAGTGAAGAGGCGCTTCGGGTTGTAAGCTCTTTCACTGAGAGA 420  
 DB 361 CAGCAATGCGCGTGAAGTGAAGAGGCGCTTCGGGTTGTAAGCTCTTTCACTGAGAGA 420

QY 421 AAAGGTTACGGTAAATAATCGTGACTCATGACGGTATCGACAGAAAGCAACCGGCTAAC 480  
 DB 421 AAAGGTTACGGTAAATAATCGTGACTCATGACGGTATCGACAGAAAGCAACCGGCTAAC 480

QY 481 TACGTGCCAGCAGCCGCGTAAATACGTAGGGTCAAGCGCTTAATCGGAATTACTGGCGT 540  
 DB 481 TACGTGCCAGCAGCCGCGTAAATACGTAGGGTCAAGCGCTTAATCGGAATTACTGGCGT 540

QY 541 AAAGGTTGCGAGCGCGCTTTGTAAGTCAAGTGAATATCCCGGGCTTAACTGGGAAT 600  
 DB 541 AAAGGTTGCGAGCGCGCTTTGTAAGTCAAGTGAATATCCCGGGCTTAACTGGGAAT 600

QY 601 TCGGTTTGAATCTCAAGGCTAGAGTGGCGAGGAGGTGGAATTCATCTGTAGCAG 660  
 DB 601 TCGGTTTGAATCTCAAGGCTAGAGTGGCGAGGAGGTGGAATTCATCTGTAGCAG 660

QY 661 TGAATTCGTAGAGATATCGAAGAAATCATCGATGGGAGGAGCGCTTCTGGGTAACT 720  
 DB 661 TGAATTCGTAGAGATATCGAAGAAATCATCGATGGGAGGAGCGCTTCTGGGTAACT 720

QY 721 GACGCTCATGCAAGAGCGTGGGAGCAAAACAGGATTAGATACCTGTGTAGTCCACGCC 780  
 DB 721 GACGCTCATGCAAGAGCGTGGGAGCAAAACAGGATTAGATACCTGTGTAGTCCACGCC 780

QY 781 CTAAGGATGTCACTAGTGTGGGCTTATAGGCTTGGTAAACGAGCTAACCGGTGA 840  
 DB 781 CTAAGGATGTCACTAGTGTGGGCTTATAGGCTTGGTAAACGAGCTAACCGGTGA 840

DB 781 CTAAGGATGTCACTAGTGTGGGCTTATAGGCTTGGTAAACGAGCTAACCGGTGA 840  
 QY 841 AGTTGACCGCTGGGAGTACGGTTCGCAAGATTAATACTCAAGGAAATTTGACGGGACCC 900  
 DB 841 AGTTGACCGCTGGGAGTACGGTTCGCAAGATTAATACTCAAGGAAATTTGACGGGACCC 900

QY 901 GCACAGCGGTGGATTAATGATGATTAATTCGATGCAACGCGAAGAACTTACTACCTT 960  
 DB 901 GCACAGCGGTGGATTAATGATGATTAATTCGATGCAACGCGAAGAACTTACTACCTT 960

QY 961 GACATGTAGCGAATTTCTAGAGATAGATTTAGTGTCTCGGGAACCTTAACACAGGTGCTG 1020  
 DB 961 GACATGTAGCGAATTTCTAGAGATAGATTTAGTGTCTCGGGAACCTTAACACAGGTGCTG 1020

QY 1021 CATGCTGTCTGACGCTCGTGTGATGATGTTGGGTTAAGTCCCGCAACGAGCGCAACC 1080  
 DB 1021 CATGCTGTCTGACGCTCGTGTGATGATGTTGGGTTAAGTCCCGCAACGAGCGCAACC 1080

QY 1081 CTTGTCAATTAATGCGATCAATTTGGTTGGGCACATTTAATGAGACTGCCGGTCAACAACG 1140  
 DB 1081 CTTGTCAATTAATGCGATCAATTTGGTTGGGCACATTTAATGAGACTGCCGGTCAACAACG 1140

QY 1141 GAGGAAGTGGGATGACGTCAAGTCTCATGGCCCTTATGGGTAGGCTTCAACGTA 1200  
 DB 1141 GAGGAAGTGGGATGACGTCAAGTCTCATGGCCCTTATGGGTAGGCTTCAACGTA 1200

QY 1201 TACAATGCGCGTACAGAGGTTGCAACCCCGAGGGGAGCTAATCTCAGAAAAGCGCG 1260  
 DB 1201 TACAATGCGCGTACAGAGGTTGCAACCCCGAGGGGAGCTAATCTCAGAAAAGCGCG 1260

QY 1261 TCGTAGTCCGATCGGAGTCTGCAACTCGACTCGGTGAAGTCGGAATCGCTAGTAATCGC 1320  
 DB 1261 TCGTAGTCCGATCGGAGTCTGCAACTCGACTCGGTGAAGTCGGAATCGCTAGTAATCGC 1320

QY 1321 GGATCAGCATGTGCGGGTGAATACGTTCCCGGCTCTGTACACACCGCCCGTCAACCAT 1380  
 DB 1321 GGATCAGCATGTGCGGGTGAATACGTTCCCGGCTCTGTACACACCGCCCGTCAACCAT 1380

QY 1381 GGGAGTGGGTTTACCAGAACGAGTACTTAACCGTAAAGAGGGCGCTTGGCCACGGTGA 1440  
 DB 1381 GGGAGTGGGTTTACCAGAACGAGTACTTAACCGTAAAGAGGGCGCTTGGCCACGGTGA 1440

QY 1441 GATTCAATGACCTGGGTG 1457  
 DB 1441 GATTCAATGACCTGGGTG 1457

RESULT 2  
 ADM32704  
 ID ADM32704 standard; DNA; 1457 BP.  
 XX  
 AC ADM32704;  
 XX  
 DT 17-JUN-2004 (first entry)  
 XX  
 DE AOB Type A R7clone140 16S rDNA.  
 XX  
 KW 16S rDNA; ammonia oxidising bacteria; AOB; ammonia; nitrite;  
 KW aqueous environment; freshwater; seawater; aquarium; ss.  
 XX  
 OS Nitrosomonas sp.  
 XX  
 PN WO2004026772-A2.  
 XX  
 PD 01-APR-2004.  
 XX  
 PF 10-SEP-2003; 2003WO-US028210.  
 XX  
 PR 19-SEP-2002; 2002US-0386217P.  
 PR 19-SEP-2002; 2002US-0386218P.  
 PR 19-SEP-2002; 2002US-0386219P.  
 XX  
 PA (AQUA-) AQUARIA INC.



XX Hovanec TA;  
XX WPI; 2004-304936/28.  
XX  
XX New composition comprising an isolated bacterial strain that oxidizes  
XX ammonia to nitrite, useful for alleviating or preventing the accumulation  
XX of ammonia in aqueous environment.  
XX  
XX Disclosure; Page 8-9; 98pp; English.  
XX  
XX This sequence represents a 16S rDNA sequence derived from an ammonia  
XX oxidising bacteria (AOB). This sequence may be used in a composition  
XX which comprises an isolated bacterial strain that oxidizes ammonia to  
XX nitrite. The composition may be used for alleviating or preventing the  
XX accumulation of ammonia in a medium. The ammonia is reduced by at least  
XX 30% when compared with a level of ammonia that would exist in the absence  
XX of the bacterial strain. The composition is useful for alleviating or  
XX preventing the accumulation of ammonia in aqueous environment, e.g. a  
XX freshwater or seawater aquarium.  
XX  
XX Sequence 1457 BP; 378 A; 315 C; 456 G; 308 T; 0 U; 0 Other;  
XX  
XX Query Match 100.0%; Score 1457; DB 12; Length 1457;  
XX Best Local Similarity 100.0%; Pred. No. 0;  
XX Matches 1457; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX 1 ATTGAACGCTGGCGCATGCTTTACACATGCAAGTCAAGCGACGCGGATGCTTCAT 60  
XX  
XX 1 ATTGAACGCTGGCGCATGCTTTACACATGCAAGTCAAGCGACGCGGATGCTTCAT 60  
XX  
XX 61 CTGTGGGAGTGGCGAGCGGTGAGTAAATCGATCGGAACGATATCCAGAGAGGGGTA 120  
XX  
XX 61 CTGTGGGAGTGGCGAGCGGTGAGTAAATCGATCGGAACGATATCCAGAGAGGGGTA 120  
XX  
XX 121 ACGCATCGAAAGATGTCTAATACCGCATATCTTAAGGAGGAAAGCAGGGGATCGAAA 180  
XX  
XX 121 ACGCATCGAAAGATGTCTAATACCGCATATCTTAAGGAGGAAAGCAGGGGATCGAAA 180  
XX  
XX 181 GACCTTGGCGCTTTGGAGCGCGCATGCTCTCATAGCTAGTTGGTGGGTAAGGCGCTAC 240  
XX  
XX 241 CAAGCGACGATCAGTAGTGGTCTGAGAGACGACCGACCGACCTGGGACTGAGACAG 300  
XX  
XX 241 CAAGCGACGATCAGTAGTGGTCTGAGAGACGACCGACCGACCTGGGACTGAGACAG 300  
XX  
XX 301 GCCCAGACTCTACGGGAGGCGAGTGGGAAATTTTGGCAATGGGCGCAAGCGCTGATC 360  
XX  
XX 301 GCCCAGACTCTACGGGAGGCGAGTGGGAAATTTTGGCAATGGGCGCAAGCGCTGATC 360  
XX  
XX 361 CAGCAATGCCCGTGAGTGAAGAGGCGCTCGGGTTGTAAAGCTCTTTTCACTCGAGAAGA 420  
XX  
XX 361 CAGCAATGCCCGTGAGTGAAGAGGCGCTCGGGTTGTAAAGCTCTTTTCACTCGAGAAGA 420  
XX  
XX 421 AAAGGTTACGGTAAATATCTGACTCATGACGGTATCGACAGAGACGACCGGCTTAAC 480  
XX  
XX 421 AAAGGTTACGGTAAATATCTGACTCATGACGGTATCGACAGAGAGACGACCGGCTTAAC 480  
XX  
XX 481 TACGTGCCAGCAGCGCGGTAAATACGTAGGCTGCAAGCGTTAAATCGGAATTTACTTGGCGGT 540  
XX  
XX 481 TACGTGCCAGCAGCGCGGTAAATACGTAGGCTGCAAGCGTTAAATCGGAATTTACTTGGCGGT 540  
XX  
XX 541 AAAGGGTGGCGAGCGCGCTTTTGAAGTCAAGTGTCAAAATCCCGGGCTTAACTTGGGAAT 600  
XX  
XX 541 AAAGGGTGGCGAGCGCGCTTTTGAAGTCAAGTGTCAAAATCCCGGGCTTAACTTGGGAAT 600  
XX  
XX 601 TCGTTTTGAACACTACAGGCTTAGAGTGGCAGAGGAGGTGGAAATTCATCTGTAGCAG 660  
XX  
XX 601 TCGTTTTGAACACTACAGGCTTAGAGTGGCAGAGGAGGTGGAAATTCATCTGTAGCAG 660  
XX  
XX 661 TGAATCGTAGATATGGAAGAACATCGATGCGAGGCGAGCTCTCTGGTTTAACTACT 720  
XX  
XX

Db 661 TGAATCGTAGATATGGAAGAACATCGATGCGAGGCGAGCGCTCTCTGGTTTAACTACT 720  
Qy 721 GAGCCTCATGACGAAAGCGTGGGAGCAAAACAGGATTAGATACCTCTGGTAGTCCAGCC 780  
Db 721 GAGCCTCATGACGAAAGCGTGGGAGCAAAACAGGATTAGATACCTCTGGTAGTCCAGCC 780  
Qy 781 CTAAACGATGCTCAACTAGTTGTTGGGCTTTATTAGGCTTGTACGAAGCTTAACGCGTGA 840  
Db 781 CTAAACGATGCTCAACTAGTTGTTGGGCTTTATTAGGCTTGTACGAAGCTTAACGCGTGA 840  
Qy 841 AGTTGACCGCTCGGGAGTACGGTTCGCAAGATTAATAAATCTCAAGGAATTTGCGGGGACCC 900  
Db 841 AGTTGACCGCTCGGGAGTACGGTTCGCAAGATTAATAAATCTCAAGGAATTTGCGGGGACCC 900  
Qy 901 GCACAAGCGGTGATGATTTGATGGAATTAATTCGATCAACGCGAAGAACTTACCTACCCCTT 960  
Db 901 GCACAAGCGGTGATGATTTGATGGAATTAATTCGATCAACGCGAAGAACTTACCTACCCCTT 960  
Qy 961 GACATGTAGCGAAATTTTCTAGAGATAGATTTAGTGTCTTGGGAAACGCTTAACACAGTGTCTG 1020  
Db 961 GACATGTAGCGAAATTTTCTAGAGATAGATTTAGTGTCTTGGGAAACGCTTAACACAGTGTCTG 1020  
Qy 1021 CATGGCTGTCTGAGCTCGTGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACC 1080  
Db 1021 CATGGCTGTCTGAGCTCGTGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACC 1080  
Qy 1081 CTTGTCTAATTAATTTGCCATCATTTTGGTTGGGCACTTTAATGAGACTGCGCGGTGACAAACCG 1140  
Db 1081 CTTGTCTAATTAATTTGCCATCATTTTGGTTGGGCACTTTAATGAGACTGCGCGGTGACAAACCG 1140  
Qy 1141 GAGAAAGTGGGAGTACGCTCAAGTCTCTCATGCTCTTATGGGTAGGCTTACACAGTAA 1200  
Db 1141 GAGAAAGTGGGAGTACGCTCAAGTCTCTCATGCTCTTATGGGTAGGCTTACACAGTAA 1200  
Qy 1201 TACAATGGCGCGTACAGAGGTTGCCAAACCGGAGGGGAGCTAAATCTCAGAAAGCGCG 1260  
Db 1201 TACAATGGCGCGTACAGAGGTTGCCAAACCGGAGGGGAGCTAAATCTCAGAAAGCGCG 1260  
Qy 1261 TCGTAGTCCGGATCGGAGTCTGCAACTCGACTCGCTGGAAGTCCGAATCGCTAGTAAATCGC 1320  
Db 1261 TCGTAGTCCGGATCGGAGTCTGCAACTCGACTCGCTGGAAGTCCGAATCGCTAGTAAATCGC 1320  
Qy 1321 GGATCAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCGCTCACACCAT 1380  
Db 1321 GGATCAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCGCTCACACCAT 1380  
Qy 1381 GGGAGTGGGTTTCCACAGAGCAGGTTAGTCTAACCGTAAAGAGGGCGCTTGGCCACGGTGA 1440  
Db 1381 GGGAGTGGGTTTCCACAGAGCAGGTTAGTCTAACCGTAAAGAGGGCGCTTGGCCACGGTGA 1440  
Qy 1441 GATTCTAGCTGGGGTG 1457  
Db 1441 GATTCTAGCTGGGGTG 1457

## RESULT 3

ABA02417  
ID ABA02417 standard; DNA; 1457 BP.  
XX  
XX ABA02417;  
XX  
XX  
XX 29-AUG-2003 (revised)  
XX 04-MAR-2002 (first entry)  
XX  
XX Type A1 ammonia-oxidising bacterium 16S rRNA gene sequence, R7clone187.  
XX Type A1; ammonia-oxidising bacterium; AOB; nitrite; 16S rRNA gene;  
XX ribosomal RNA; aquarium; aquaculture; waste water treatment;  
XX bioremediation; ds.  
XX Nitrosomonadales.  
XX  
XX WO200190312-A1.  
PN

XX 29-NOV-2001.  
 XX PD  
 XX PF 17-MAY-2001; 2001WO-US016265.  
 XX PR 19-MAY-2000; 2000US-00573684.  
 XX (AQUA-) AQUARIA INC.  
 XX PI Hovanec TA, Burrell PC;  
 XX DR WPI; 2002-075367/10.  
 XX PT New bacteria capable of oxidizing ammonia to nitrite, for preventing or  
 XX PT alleviating the accumulation of ammonia in fresh water aquaria, seawater  
 XX PT aquaria and waste water.  
 XX PS Claim 2; Page 6; 62pp; English.  
 CC The invention relates to 4 novel types of ammonia-oxidising bacteria  
 CC (AOB) found in freshwater aquaria. The bacteria are able to oxidise  
 CC ammonia to nitrite and are members of the ammonia-oxidising bacteria  
 CC family of the beta subdivision of Proteobacteria. The 4 types of bacteria  
 CC can be distinguished on the basis of their 16S rRNA (ribosomal RNA) gene  
 CC sequences (ABA02416-ABA02419), and are classified as AOB type A (e.g.,  
 CC R7clone140), type A1 (e.g., R7clone187), type B (e.g., R3clone5) and type  
 CC C (e.g., R3clone47). The invention also encompasses isolated 16S rRNA  
 CC gene sequences of the ammonia-oxidising bacteria of the invention,  
 CC oligonucleotide probes and primers for the detection of these bacteria,  
 CC and compositions comprising the bacteria. The bacteria of the invention  
 CC are useful in biological filters for reducing ammonia accumulation in  
 CC both freshwater and seawater aquaria. They may also be used in waste  
 CC water treatment and in bioremediation processes to reduce the level of  
 CC pollution caused by ammonia. The present sequence represents R7clone187,  
 CC a 16S rRNA gene sequence from the type A1 ammonia-oxidising bacterium of  
 CC the invention. (Updated on 29-AUG-2003 to standardise OS field)  
 XX  
 SQ Sequence 1457 BP; 379 A; 317 C; 455 G; 306 T; 0 U; 0 Other;  
 Query Match 99.7%; Score 1452.2; DB 6; Length 1457;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 1454; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 ATTGACCTGGCGCATGCTTACACATGCAAGTCGAACCGCAGCAGGATGCTGCAT 60  
 DB 1 ATTGACCTGGCGCATGCTTACACATGCAAGTCGAACCGCAGCAGGATGCTGCAT 60  
 QY 61 CTGGTGGCGAGTGGCGGACGGGTGAGTAAATGATCGGAACGATATCCAGAGAGGGGGTA 120  
 DB 61 CTGGTGGCGAGTGGCGGACGGGTGAGTAAATGATCGGAACGATATCCAGAGAGGGGGTA 120  
 QY 121 ACGCATCGAAAGATGTGTATACCGCATATATCTTAAGAGGAGAAAGCAGGGGATCGAAA 180  
 DB 121 ACGCATCGAAAGATGTGTATACCGCATATATCTTAAGAGGAGAAAGCAGGGGATCGAAA 180  
 QY 181 GACCTTGGCTTTTGGAGCGCGCATGCTGATAGTCTGATAGTCTGATAGTCTGATAGTCTGAT 240  
 DB 181 GACCTTGGCTTTTGGAGCGCGCATGCTGATAGTCTGATAGTCTGATAGTCTGATAGTCTGAT 240  
 QY 241 CAAGCGGACGATCAGTAGTGTGTGAGAGGACGACCGACACACTGGGACTGAGACACG 300  
 DB 241 CAAGCGGACGATCAGTAGTGTGTGAGAGGACGACCGACACACTGGGACTGAGACACG 300  
 QY 301 GCCCAGACTCTTACGGGAGGACGATGCGGGAATTTTGGACAATTTGGCGCGCAAGCTGATC 360  
 DB 301 GCCCAGACTCTTACGGGAGGACGATGCGGGAATTTTGGACAATTTGGCGCGCAAGCTGATC 360  
 QY 361 CAGCAATCCCGCTGAGTGAAGAGGCCCTTCGGGTGTAAAGCTCTTTCAGTCGAGAGA 420  
 DB 361 CAGCAATCCCGCTGAGTGAAGAGGCCCTTCGGGTGTAAAGCTCTTTCAGTCGAGAGA 420  
 QY 421 AAAGGTTACGGTAAATATCGTGACTCATGCGGTATCGACGAAGAGGACCGCGCTAAC 480

DB 421 AAAGGTTACGGTAAATATCGTGACCCATCGACGGTATCGACAGAGGACCGCGCTAAC 480  
 QY 481 TACGTGCAGCAGCGCGGTAAATACGTAGGTGCAAGCGTTAATCGGAATTTACTGGCGT 540  
 DB 481 TACGTGCAGCAGCGCGGTAAATACGTAGGTGCAAGCGTTAATCGGAATTTACTGGCGT 540  
 QY 541 AAAGGGTGGCAGCGCGCTTTGTAAGTCAGATGTGAATCCCGGGCTTAACTTGGGAAT 600  
 DB 541 AAAGGGTGGCAGCGCGCTTTGTAAGTCAGATGTGAATCCCGGGCTTAACTTGGGAAT 600  
 QY 601 TGCCTTTGAAACTACAAGGCTAGAGTGTGGCAGAGGAGGTGGAATTCATGTGTAGCAG 660  
 DB 601 TGCCTTTGAAACTACAAGGCTAGAGTGTGGCAGAGGAGGTGGAATTCATGTGTAGCAG 660  
 QY 661 TGAATCGGTAGAGATATGAAGAACATCGATGCGGAGGAGGCTCTCTGGTTAACTACT 720  
 DB 661 TGAATCGGTAGAGATATGAAGAACATCGATGCGGAGGAGGCTCTCTGGTTAACTACT 720  
 QY 721 GACGCTCATGCAAGAGCGTGGGAGCAACAGGATTTAGATACCTCTGGTAGTCCACGCC 780  
 DB 721 GACGCTCATGCAAGAGCGTGGGAGCAACAGGATTTAGATACCTCTGGTAGTCCACGCC 780  
 QY 781 CTRAACGATGTCAACTAGTTGTTGGGCTTTATTAGGCTTGTAAACGAAGCTAACCGGTGA 840  
 DB 781 CTRAACGATGTCAACTAGTTGTTGGGCTTTATTAGGCTTGTAAACGAAGCTAACCGGTGA 840  
 QY 841 AGTTGACCGCTGGGAGTACGCTCGCAAGATTTAAACTCAAAGGAATTTGACGGGACCC 900  
 DB 841 AGTTGACCGCTGGGAGTACGCTCGCAAGATTTAAACTCAAAGGAATTTGACGGGACCC 900  
 QY 901 GCACAAGCGGTGGATTTGTTGGGCTTTATTCGATCAACGCGAAGAACTTACCTACCCCTT 960  
 DB 901 GCACAAGCGGTGGATTTGTTGGGCTTTATTCGATCAACGCGAAGAACTTACCTACCCCTT 960  
 QY 961 GACATGTAGCGAAATTTCTAGAGATAGATTTAGTCTTTCGGGAACTGTAACAGAGTGTG 1020  
 DB 961 GACATGTAGCGAAATTTCTAGAGATAGATTTAGTCTTTCGGGAACTGTAACAGAGTGTG 1020  
 QY 1021 CATGGCTGTGTCAGCTCGTGTGATGATGTTGGGTTAAGTCCCGCAACGAGCGCAACC 1080  
 DB 1021 CATGGCTGTGTCAGCTCGTGTGATGATGTTGGGTTAAGTCCCGCAACGAGCGCAACC 1080  
 QY 1081 CTGTGCTAATTAATTTGCCATCATTTGTTGGGCACTTTAATGAGACTGCGGTGACAAACCG 1140  
 DB 1081 CTGTGCTAATTAATTTGCCATCATTTGTTGGGCACTTTAATGAGACTGCGGTGACAAACCG 1140  
 QY 1141 GAGGAAGGTGGGATGACGTCAGTCTCATGCGCTTTATGGGTAGGGCTTTCAACGTTAA 1200  
 DB 1141 GAGGAAGGTGGGATGACGTCAGTCTCATGCGCTTTATGGGTAGGGCTTTCAACGTTAA 1200  
 QY 1201 TACATGGCGGTACAGAGGTTTCCCAACCGCGGAGGGGAGCTAATCTCAGAAAGCGCG 1260  
 DB 1201 TACATGGCGGTACAGAGGTTTCCCAACCGCGGAGGGGAGCTAATCTCAGAAAGCGCG 1260  
 QY 1261 TCGTAGTCCGATCGGAGTCTGCAACTCGACTCGTCAAGTCGGAATCGCTAGTAATCGC 1320  
 DB 1261 TCGTAGTCCGATCGGAGTCTGCAACTCGACTCGTCAAGTCGGAATCGCTAGTAATCGC 1320  
 QY 1321 GGATCAGCATGTCCGGTGAATACGTTCCGGGTCTTTGTACACACCGCGCTCACCAT 1380  
 DB 1321 GGATCAGCATGTCCGGTGAATACGTTCCGGGTCTTTGTACACACCGCGCTCACCAT 1380  
 QY 1381 GGGAGTGGGTTTACCAGAGGAGGATGCTTAACCGTTAAGAGGGCGCTTGGCAGCGTGA 1440  
 DB 1381 GGGAGTGGGTTTACCAGAGGAGGATGCTTAACCGTTAAGAGGGCGCTTGGCAGCGTGA 1440  
 QY 1441 GATTTCATGACTGGGGTG 1457  
 DB 1441 GATTTCATGACTGGGGTG 1457

ID AD32705 standard; DNA; 1457 BP.  
 XX AC AD32705;  
 XX ET 17-JUN-2004 (first entry)  
 XX DE AOB Type A1 R7clone187 16S rDNA.  
 XX KW 16S rDNA; ammonia oxidizing bacteria; AOB; ammonia; nitrite;  
 KW aqueous environment; freshwater; seawater; aquarium; ss.  
 XX OS Nitrosomonas sp.  
 XX PN WO2004026772-A2.  
 XX PD 01-APR-2004.  
 XX PF 10-SEP-2003; 2003WO-US028210.  
 XX PR 19-SEP-2002; 2002US-0386217P.  
 XX PR 19-SEP-2002; 2002US-0386218P.  
 XX PR 19-SEP-2002; 2002US-0386219P.  
 XX PA (AQUA-) AQUARIA INC.  
 XX PI Hovanec TA;  
 XX DR WPI; 2004-304936/28.  
 XX PT New composition comprising an isolated bacterial strain that oxidizes  
 PT ammonia to nitrite, useful for alleviating or preventing the accumulation  
 PT of ammonia in aqueous environment.  
 XX PS Disclosure; Page 10; 98pp; English.  
 XX CC This sequence represents a 16S rDNA sequence derived from an ammonia  
 CC oxidizing bacteria (AOB). This sequence may be used in a composition  
 CC which comprises an isolated bacterial strain that oxidizes ammonia to  
 CC nitrite. The composition may be used for alleviating or preventing the  
 CC accumulation of ammonia in a medium. The ammonia is reduced by at least  
 CC 30% when compared with a level of ammonia that would exist in the absence  
 CC of the bacterial strain. The composition is useful for alleviating or  
 CC preventing the accumulation of ammonia in aqueous environment, e.g. a  
 CC freshwater or seawater aquarium.  
 XX SQ Sequence 1457 BP; 379 A; 317 C; 455 G; 306 T; 0 U; 0 Other;  
 Query Match 99.7%; Score 1452.2; DB 12; Length 1457;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 1454; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 ATTGAACGCTGGCGCATGCTTTACACATGCAAGTCGAACGCGACGCGATGCTTGCAT 60  
 DB 1 ATTGAACGCTGGCGCATGCTTTACACATGCAAGTCGAACGCGACGCGATGCTTGCAT 60  
 QY 61 CTGTGGCGAGTGGCGGACGGGTGAGTAATGCAATCGGAACGTATCCAGAGGGGGTA 120  
 DB 61 CTGTGGCGAGTGGCGGACGGGTGAGTAATGCAATCGGAACGTATCCAGAGGGGGTA 120  
 QY 121 ACGCATCGAAGATGTGCTAATACCGCATATCTCTAAGGAGGAAGCAGGGGATCGAAA 180  
 DB 121 ACGCATCGAAGATGTGCTAATACCGCATATCTCTAAGGAGGAAGCAGGGGATCGAAA 180  
 QY 181 GACCTTGGCTTTTGGAGCGGCCGATGTCATGCTAGCTAGTGTGGGTAAAGCCCTAC 240  
 DB 181 GACCTTGGCTTTTGGAGCGGCCGATGTCATGCTAGCTAGTGTGGGTAAAGCCCTAC 240  
 QY 241 CAAGCGGACGATCAGTAGTGTGCTGAGAGGACGACCGACACTGGGACTGAGACAG 300  
 DB 241 CAAGCGGACGATCAGTAGTGTGCTGAGAGGACGACCGACACTGGGACTGAGACAG 300  
 QY 301 GCCCAGACTCTACGGGAGGCGAGTGGGNAATTTTGGACAATGGGCGCAAGCCTGATC 360  
 DB 301 GCCCAGACTCTACGGGAGGCGAGTGGGNAATTTTGGACAATGGGCGCAAGCCTGATC 360

DB 301 GCCCAGACTCTACGGGAGGCGAGTGGGNAATTTTGGACAATGGGCGCAAGCCTGATC 360  
 QY 361 CAGCAATGCCGCGTGAAGTGAAGAGGCTTCGGGTTGTAAAGCTCTTTTCAGTCGAGAAGA 420  
 DB 361 CAGCAATGCCGCGTGAAGTGAAGAGGCTTCGGGTTGTAAAGCTCTTTTCAGTCGAGAAGA 420  
 QY 421 AAAGGTTACGGTAAATATCGTGAATCATGACGCTATCGACAGAAAGACCGGCTAAC 480  
 DB 421 AAAGGTTACGGTAAATATCGTGAATCATGACGCTATCGACAGAAAGACCGGCTAAC 480  
 QY 481 TACGTGCCAGCAGCCGCGTAATACGTAGGTCAAGCGTTAAATCGGAATTTACTGGGCGT 540  
 DB 481 TACGTGCCAGCAGCCGCGTAATACGTAGGTCAAGCGTTAAATCGGAATTTACTGGGCGT 540  
 QY 541 AAAGGTTGCCAGCGGCTTTTGAAGTCAGATGTAATCCCGGGCTTAACCTGGGAAT 600  
 DB 541 AAAGGTTGCCAGCGGCTTTTGAAGTCAGATGTAATCCCGGGCTTAACCTGGGAAT 600  
 QY 601 TGGCTTTGAAACTACAAGGCTAGAGTGTGGCAGAGGAGGTGGAAATCCATGTGTAGCAG 660  
 DB 601 TGGCTTTGAAACTACAAGGCTAGAGTGTGGCAGAGGAGGTGGAAATCCATGTGTAGCAG 660  
 QY 661 TGAATCGGTAGAGATATGGAAGAACATCGATGCGGAAGGCGGCTCTCTGGTTAAACACT 720  
 DB 661 TGAATCGGTAGAGATATGGAAGAACATCGATGCGGAAGGCGGCTCTCTGGTTAAACACT 720  
 QY 721 GACGCTCATGCAAGAAAGCGTGGGAGCAACAGGATAGATACCTGGTGTAGTCCAGGCC 780  
 DB 721 GACGCTCATGCAAGAAAGCGTGGGAGCAACAGGATAGATACCTGGTGTAGTCCAGGCC 780  
 QY 781 CTAACCATGTCACATAGTTGTTGGGCTTATTAAGGCTTGGTAAACGAGCTAAACGCGTGA 840  
 DB 781 CTAACCATGTCACATAGTTGTTGGGCTTATTAAGGCTTGGTAAACGAGCTAAACGCGTGA 840  
 QY 841 AGTTGACCGCTCGGGAGTACGCTCGCAAGATTAATACTCAAAGGAATGACGGGACCC 900  
 DB 841 AGTTGACCGCTCGGGAGTACGCTCGCAAGATTAATACTCAAAGGAATGACGGGACCC 900  
 QY 901 GCACAAGCGGTGATTTATGGAATTAATTCATGCAACGCGGAAAAACCTTACCTACCCCTT 960  
 DB 901 GCACAAGCGGTGATTTATGGAATTAATTCATGCAACGCGGAAAAACCTTACCTACCCCTT 960  
 QY 961 GACATGTAGCGAAATTTCTAGAGATAGATAGTCTCTCGGGAACGCTAAACACAGTGTGTG 1020  
 DB 961 GACATGTAGCGAAATTTCTAGAGATAGATAGTCTCTCGGGAACGCTAAACACAGTGTGTG 1020  
 QY 1021 CATGGCTGTGCTCAGCTCGTGTGCTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACC 1080  
 DB 1021 CATGGCTGTGCTCAGCTCGTGTGCTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACC 1080  
 QY 1081 CTTGTCTAATTAATGCGCATCAATTTGGTTGGGCACTTTAATGAGACTGCGGTTGACAAACCG 1140  
 DB 1081 CTTGTCTAATTAATGCGCATCAATTTGGTTGGGCACTTTAATGAGACTGCGGTTGACAAACCG 1140  
 QY 1141 GAGGAAGTGGGATGACGTCAGTCTCTCATGGCCCTTATGGGTAGGCTTTACACGTA 1200  
 DB 1141 GAGGAAGTGGGATGACGTCAGTCTCTCATGGCCCTTATGGGTAGGCTTTACACGTA 1200  
 QY 1201 TACAATGGCGGTACAGAGGGTTGCAACCCCGAGGGGGAGCTAATCTCAGAAGCGCG 1260  
 DB 1201 TACAATGGCGGTACAGAGGGTTGCAACCCCGAGGGGGAGCTAATCTCAGAAGCGCG 1260  
 QY 1261 TCGTAGTCCGGATCGGAGTCTGCAACTCGACTCGTGAAGTCGGAATCGCTAGTAATCGC 1320  
 DB 1261 TCGTAGTCCGGATCGGAGTCTGCAACTCGACTCGTGAAGTCGGAATCGCTAGTAATCGC 1320  
 QY 1321 GGATCAGCATGTCGCGGTGAATAGTTCCCGGGTCTTGTACACACCGCCCTCACACCAT 1380  
 DB 1321 GGATCAGCATGTCGCGGTGAATAGTTCCCGGGTCTTGTACACACCGCCCTCACACCAT 1380  
 QY 1381 GGGAGTGGGTTTCCACAGAAAGCAGGTAGTCTAAACCGTAAAGGAGGGCGCTTGGCCACGGTGA 1440  
 DB 1381 GGGAGTGGGTTTCCACAGAAAGCAGGTAGTCTAAACCGTAAAGGAGGGCGCTTGGCCACGGTGA 1440



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Dy 1320 CGGATCAGCATGTCGGCGTGATACGTTCCCGGTCCTTGTACACACCGCGGTACACCA 1379
Db 1338 CGGATCAGCATGTCGGCGTGATACGTTCCCGGTCCTTGTACACACCGCGGTACACCA 1397
Dy 1380 TGGGAGTGGGTTTACACAGAAGCAGGTAGTCTTAACCGTAAGGAGGGCGCTTGGCACCGGTG 1439
Db 1398 TGGGAGTGGGTTTACACAGAAGCAGGTAGTCTTAACCGTAAGGAGGGCGCTTGGCACCGGTG 1457
Dy 1440 AGATTATGACTGGGGTG 1457
Db 1458 AGATTATGACTGGGGTG 1475

RESULT 6
ADM32722
ID ADM32722 standard; DNA; 1494 BP.
XX
AC ADM32722;
XX
DT 17-JUN-2004 (first entry)
XX
XX AOB P4clone31 16S rDNA.
XX DE 16S rDNA; ammonia oxidising bacteria; AOB; ammonia; nitrite;
XX KW aqueous environment; freshwater; seawater; aquarium; ss.
XX KW
XX OS Nitrosomonas aestuarii.
XX PN W02004026772-A2.
XX XX
XX PD 01-APR-2004.
XX PF 10-SEP-2003; 2003WO-US028210.
XX PR 19-SEP-2002; 2002US-0386217P.
XX PR 19-SEP-2002; 2002US-0386218P.
XX PR 19-SEP-2002; 2002US-0386219P.
XX XX
XX PA (AQUA-) AQUARIA INC.
XX PI Hovanec TA;
XX XX
XX DR WPI; 2004-304936/28.
XX
XX PT New composition comprising an isolated bacterial strain that oxidizes
XX PT ammonia to nitrite, useful for alleviating or preventing the accumulation
XX PT of ammonia in aqueous environment.
XX XX
XX PS Claim 1; Page 14; 98pp; English.
XX
XX CC This sequence represents a 16S rDNA sequence derived from an ammonia
XX CC oxidizing bacteria (AOB). This sequence may be used in a composition
XX CC which comprises an isolated bacterial strain that oxidizes ammonia to
XX CC nitrite. The composition may be used for alleviating or preventing the
XX CC accumulation of ammonia in a medium. The ammonia is reduced by at least
XX CC 30% when compared with a level of ammonia that would exist in the absence
XX CC of the bacterial strain. The composition is useful for alleviating or
XX CC preventing the accumulation of ammonia in aqueous environment, e.g. a
XX CC freshwater or seawater aquarium.
XX XX
XX SQ Sequence 1494 BP; 392 A; 327 C; 459 G; 316 T; 0 U; 0 Other;

Query Match 93.3%; Score 1359.2; DB 12; Length 1494;
Best Local Similarity 96.3%; Pred. No. 0;
Matches 1402; Conservative 0; Mismatches 53; Indels 1; Gaps 1;

QY 1 ATTGAACGCTGGCGGATGCTTTACATGCAATCGAACGGGACGAGATGCTTGCAT 60
Db 19 ATTGAACGCTGGCGGATGCTTTACATGCAATCGAACGGGACGAGCTGCTGCAC 78
QY 61 CTGGTGGGAGTGGCGGACGGGTGATGCAATCGAACGGGACGAGATGCTTGCAT 120

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Db 79 CTGCTGGCGAGTGGCGGACGGGTAGTAATGCATCGGAACTGTCCGGAAGTGGGGGATA 138
QY 121 ACGCATCGAAAGATGCTCTAATACCGCATATATCTCTAAGAGGAAAGCAGGGGATCGAAA 180
Db 139 ACGCATCGAAAGATGCTCTAATACCGCATATATCTCTAAGAGGAAAGCAGGGGATCGAAA 198
QY 181 GACCTTCGCGCTTTTGGAGCGCGCATGCTCTGATTAGCTAGTTGGTGGGTAAGGSCCTTAC 240
Db 199 GACCTTCGCGCTTTTGGAGCGCGCATGCTCTGATTAGCTAGTTGGTGGGTAAGGSCCTTAC 258
QY 241 CAAGCGCAGCATCAGTATGTTGGTCTGAGAGGACACCGACGACACCTGGGACTGAGACACG 300
Db 259 CAAGCGCAGCATCAGTATGTTGGTCTGAGAGGACACCGACGACACCTGGGACTGAGACACG 318
QY 301 GCCCAGACTCTCTACGGGAGGACGAGTGGGGAATTTTGGACAATGGGGCGCAGCCTGATC 360
Db 319 GCCCAGACTCTCTACGGGAGGACGAGTGGGGAATTTTGGACAATGGGGCGCAGCCTGATC 378
QY 361 CAGCAATGCCGCGTGAAGTGAAGAGGCGCTTCCGGTGTAAAGCTCTTTTCACTCCAGAAGA 420
Db 379 CAGCAATGCCGCGTGAAGTGAAGAGGCGCTTCCGGTGTAAAGCTCTTTTCACTCCAGAAGA 438
QY 421 AAAGGTTACGGTAAATTAATCGTGACTCATGACGCTATCGACAGAAAGCAACCGGCTAAC 480
Db 439 AAAGGTTACGGTAAATTAATCGTGACTCATGACGCTATCGACAGAAAGCAACCGGCTAAC 498
QY 481 TAGTGCCAGCAGCGCGGTAAATACGTAGGTCGACGCTTAAATCGGAATTTACTGGGGCT 540
Db 499 TAGTGCCAGCAGCGCGGTAAATACGTAGGTCGACGCTTAAATCGGAATTTACTGGGGCT 558
QY 541 AAAGGTTGCCGCGCGCTTTTGAAGTCAGATGTGAATCCCGGGCTTAACTGGGGAAT 600
Db 559 AAAGGTTGCCGCGCGCTTTTGAAGTCAGATGTGAATCCCGGGCTTAACTGGGGAAT 618
QY 601 TGGCTTTGAAACTACAAGGCTAGAGTGTGCGAGAGGAGGTGGAATTCATGTGTAGCAG 660
Db 619 TGGCTTTGAAACTACAAGGCTAGAGTGTGCGAGAGGAGGTGGAATTCATGTGTAGCAG 678
QY 661 TGAATGCGTAGAGATATGGAAGAACATCGATGCGAAGGAGCGCTCTGTTGGTTAACT 720
Db 679 TGAATGCGTAGAGATATGGAAGAACATCGATGCGAAGGAGCGCTCTGTTGGTTAACT 738
QY 721 GAGCTCATGCGAAGCGTGGGAGCAACAGGATTAGATACCTGTTAGTCCAGGCC 780
Db 739 GAGCTCATGCGAAGCGTGGGAGCAACAGGATTAGATACCTGTTAGTCCAGGCC 798
QY 781 CTAACGATGTCAACTAGTTGTTGGGCTTTATTAGGCTTGTGTAACGAAAGCTTAACGCGTGA 840
Db 799 CTAACGATGTCAACTAGTTGTTGGGCTTTATTAGGCTTGTGTAACGAAAGCTTAACGCGTGA 858
QY 841 AGTTGACCGCTGGGAGTACGGTCCGAAGATTAAACTCAAGGAATTTGACGGGAGCCC 900
Db 859 AGTTGACCGCTGGGAGTACGGTCCGAAGATTAAACTCAAGGAATTTGACGGGAGCCC 918
QY 901 GCACAGCGGTGATTTATGGAATTAATTCGATCGAAGCAACCACTTACCTACCTCTT 960
Db 919 GCACAGCGGTGATTTATGGAATTAATTCGATCGAAGCAACCACTTACCTACCTCTT 978
QY 961 GACATGTAGCGAAATTTTCTAGAGATAGATTAGTG-CTTCCGGGAACGCTAACACAGGTGCT 1019
Db 979 GACATGTAGCGAAATTTTCTAGAGATAGATTAGTG-CTTCCGGGAACGCTAACACAGGTGCT 1038
QY 1020 GCATGGTGTGTCAGCTCGTGTGAGATGTTGGTAAAGTCCCGCAACGAGCGCAAC 1079
Db 1039 GCATGGTGTGTCAGCTCGTGTGAGATGTTGGTAAAGTCCCGCAACGAGCGCAAC 1098
QY 1080 CCTTGTGATTAATTTGGCATCATTTGGTGGGCACTTTAATGAGACTCCCGGTGACAAACC 1139
Db 1099 CCTTGTGATTAATTTGGCATCATTTGGTGGGCACTTTAATGAGACTCCCGGTGACAAACC 1158
QY 1140 GGAGGAAGGTGGGGAATGACGTCAGTCCCTCATGGCCCTTATGGGTAGGGCTTACACGTA 1199
Db 1159 GGAGGAAGGTGGGGAATGACGTCAGTCCCTCATGGCCCTTATGGGTAGGGCTTACACGTA 1218

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QY 1200 ATCAATGCGGTACAGAGGTTCACACCGCGAGGGGAGCTAATCTCAGAAAGCGC 1259  
 DB 1219 ATCAATGCGGTACAGAGGTTCACACCGCGAGGGGAGCTAATCTCAGAAAGCGC 1278  
 QY 1260 GTCTAGTCGGATCGGATCTGCAACTCGACTCCGTCGAAATCGGTCAGTAATCG 1319  
 DB 1279 GTCTAGTCGGATCGGATCTGCAACTCGACTCCGTCGAAATCGGTCAGTAATCG 1338  
 QY 1320 CGGATCAGCATGTCGGGTGAATAGTTCCTCCGGTCTTGTACACACCGCGCTCACCA 1379  
 DB 1339 CGGATCAGCATGTCGGGTGAATAGTTCCTCCGGTCTTGTACACACCGCGCTCACCA 1398  
 QY 1380 TGGGAGTGGGTTTACCAGACAGGTAGTCTAACCGTAAGGAGGCGCTTGCCACGGTG 1439  
 DB 1399 TGGAGTTGGCTGCACCAAGTAGGTGTCTAACCTCGGAGGACGCTTACCACGGTG 1458  
 QY 1440 AGATTCAATGACTGGG 1455  
 DB 1459 TGGTCAATGACTGGG 1474

## RESULT 7

ADM32721  
 ID ADM32721 standard; DNA; 1467 BP.

AC ADM32721;

DT 17-JUN-2004 (first entry)

DE AOB P4clone42 16S rDNA.

KW 16S rDNA; ammonia oxidizing bacteria; AOB; ammonia; nitrite;  
 KW aqueous environment; freshwater; seawater; aquarium; ss.

OS Nitrosomonas aestuarii.

XX WO2004026772-A2.

XX 01-APR-2004.

XX 10-SEP-2003; 2003WO-US028210.

XX 19-SEP-2002; 2002US-0386217P.

XX 19-SEP-2002; 2002US-0386218P.

XX 19-SEP-2002; 2002US-0386219P.

XX (AQUA-) AQUARIA INC.

XX Hovanec TA;

XX WPI; 2004-304936/28.

XX New composition comprising an isolated bacterial strain that oxidizes  
 PT ammonia to nitrite, useful for alleviating or preventing the accumulation  
 PT of ammonia in aqueous environment.

XX Claim 1; Page 13; 98pp; English.

XX This sequence represents a 16S rDNA sequence derived from an ammonia  
 CC oxidizing bacteria (AOB). This sequence may be used in a composition  
 CC which comprises an isolated bacterial strain that oxidizes ammonia to  
 CC nitrite. The composition may be used for alleviating or preventing the  
 CC accumulation of ammonia in a medium. The ammonia is reduced by at least  
 CC 30% when compared with a level of ammonia that would exist in the absence  
 CC of the bacterial strain. The composition is useful for alleviating or  
 CC preventing the accumulation of ammonia in aqueous environment, e.g. a  
 CC freshwater or seawater aquarium.

XX Sequence 1467 BP; 384 A; 320 C; 451 G; 312 T; 0 U; 0 Other;

XX Query Match

XX Best Local Similarity 93.3%; Score 1358.8; DB 12; Length 1467;

XX Pred. No. 0;

Matches 1414; Conservative 0; Mismatches 37; Indels 3; Gaps 3;  
 QY 1 ATTGAACGCTGGCGCATGCTTTTACCATGCAAGTCGAACCGCGAGCGATGCTTGCAT 60  
 DB 16 ATTGAACGCTGGCGCATGCTTTTACCATGCAAGTCGAACCGCGAGCGATGCTTGCAC 75  
 QY 61 CTGTGTGGCGAGTGGCGAGCGGTGAGTAATCATCTGGAAACGCTATCCAGAACAGGGGGGTA 120  
 DB 76 CTGTGTGGCGAGTGGCGAGCGGTGAGTAATCATCTGGAAACGCTATCCAGAACAGGGGGGTA 135  
 QY 121 ACGCATCGAAAGATGTCTAATACCGCATATATCTTAAGGAGGAAAGCAGGGGATCGAAA 180  
 DB 136 ACGCATCGAAAGATGTCTAATACCGCATATATCTTAAGGAGGAAAGCAGGGGATCGAAA 195  
 QY 181 GACCTTGGCTTTTGGAGCGCGCATGTCTGATTTAGCTAGTTGGTGGGTTAAAGCCCTAC 240  
 DB 196 GACCTTGGCTTTTGGAGCGCGCATGTCTGATTTAGCTAGTTGGTGGGTTAAAGCCCTAC 255  
 QY 241 CAAGGCGACGATCAGTAGTTGGTCTGAGAGGACACGACGACCATCTGGGACTTGAGACACG 300  
 DB 256 CAAGGCGACGATCAGTAGTTGGTCTGAGAGGACACGACGACCATCTGGGACTTGAGACACG 315  
 QY 301 GCCCAGACTCTCTACCGGAGGCGAGTCAGTGGGAAATTTTGGCAATGGGCGCAAGCCTGATC 360  
 DB 316 GCCCAGACTCTCTACCGGAGGCGAGTCAGTGGGAAATTTTGGCAATGGGCGCAAGCCTGATC 375  
 QY 361 CAGCAATGCGCGGTGAGTGAAGAGCGCTTCGGGTTGTAAAGCTCTTTTCACTCGAAGAAGA 420  
 DB 376 CAGCAATGCGCGGTGAGTGAAGAGG--CTTCGGGTTGTAAAGCTCTTTTCACTCGAAGAAGA 434  
 QY 421 AAGGTTACGCTAATAATCGTCACTCATGACGCTATCGACAGAGGAGGACCGGCTTAAC 480  
 DB 435 AAGGTTGCTACTAATAATCACAACCTTATGATGTCGACAGAGGAGGACCGGCTTAAC 494  
 QY 481 TACGTGCCAGCAGCGCGGTAATACTGAGGTGCAAGCGTTAAATCGGAATTTACTTGGGCGT 540  
 DB 495 TACGTGCCAGCAGCGCGGTAATACTGAGGTGCAAGCGTTAAATCGGAATTTACTTGGGCGT 554  
 QY 541 AAGGTTGCGCAGCGCGCTTTGTAAGTCAGATGGAATCCCGGGCTTAACCTTGGGAAAT 600  
 DB 555 AAGGTTGCGCAGCGCGCTTTGTAAGTCAGATGGAATCCCGGGCTTAACCTTGGGAAAT 614  
 QY 601 TGGCTTTGAAACTACAAGGCTTAGAGTGTGGCAGAGGAGGTGGAATTCATGTGTAGCAG 660  
 DB 615 TGGCTTTGAAACTACAAGGCTTAGAGTGTGGCAGAGGAGGTGGAATTCATGTGTAGCAG 674  
 QY 661 TGAATCGGTAGAGATATGGAAGAACATCGATGCGAAGGAGCGCTCTGGTTTAAACACT 720  
 DB 675 TGAATCGGTAGAGATATGGAAGAACATCGATGCGAAGGAGCGCTCTGGTTTAAACACT 734  
 QY 721 GACGCTCATGACGAAAGCGTGGGAGCAACACAGGATTAGATACCTTGGTGTAGTCCAGCC 780  
 DB 735 GACGCTCATGACGAAAGCGTGGGAGCAACACAGGATTAGATACCTTGGTGTAGTCCAGCC 794  
 QY 781 CTAAACGATGCTCAACTAGTTGTTGGGCTTTATAGGCTTGTGTAACGAAGCTTAAACGCTGA 840  
 DB 795 CTAAACGATGCTCAACTAGTTGTTGGGCTTTACTAGGCTTGGTAACTAGTAACTAGTAA 854  
 QY 841 AGTTGACCGCTCGGGAGTACGGTTCGAAGATTAAAACTCAAAGGAATTGACGGGAGCC 900  
 DB 855 AGTTGACCGCTCGGGAGTACGGTTCGAAGATTAAAACTCAAAGGAATTGACGGGAGCC 914  
 QY 901 GCACACGGTGGATTATGGAATTAATTCGATGCAACCGGAAACCTTACCTTACCTT 960  
 DB 915 GCACACGGTGGATTATGGAATTAATTCGATGCAACCGGAAACCTTACCTTACCTT 974  
 QY 961 GACATGTAGCGAATTTTCTAGAGATAGATTAGTGC--TTCCGGGAACGCTTAAACACAGGTGCT 1019  
 DB 975 GACATGTAGCGAATTTTCTAGAGATAGATTAGTGCCTTCGGGAACGCTTAAACACAGGTGCT 1034  
 QY 1020 GCATGGCTGCTCAGCTCGTGTGAGATGTTGGTGTAAAGTCCCGCAACGAGCGCAAC 1079  
 DB 1035 GCATGGCTGCTCAGCTCGTGTGAGATGTTGGTGTAAAGTCCCGCAACGAGCGCAAC 1094

QY 1080 CCTGTGATTAATGCGATCATTTGGTGGGCACTTTAATGAGACTGCCGGTGACAAACC 1139  
 DB 1095 CCTGTGATTAATGCGATCATTTGGTGGGCACTTTAATGAGACTGCCGGTGACAAACC 1154  
 QY 1140 GGAGGAAGGTGGGGATGACGTCAGTCCTCATGGCCCTTATGGTAGGGCTTCACACGTA 1199  
 DB 1155 GGAGGAAGGTGGGGATGACGTCAGTCCTCATGGCCCTTATGGTAGGGCTTCACACGTA 1214  
 QY 1200 ATCAATGGCGGTACAGAGGGTTGCCAACCCGCGAGGGGAGCTAATTCAGAAAGCGC 1259  
 DB 1215 ATCAATGGCGGTACAGAGGGTTGCCAACCCGCGAGGGGAGCTAATTCAGAAAGCGC 1274  
 QY 1260 GTGCTAGTCGGATCGAGTCGCACTCGACTCCGTGAAGTCGGAATCGTAGTAATCG 1319  
 DB 1275 GTGCTAGTCGGATCGAGTCGCACTCGACTCCGTGAAGTCGGAATCGTAGTAATCG 1334  
 QY 1320 CGGATCAGCATGTCGGGGTGAATACGTTCCCGGGTCTTTGTACACACCGCCGCTCACACCA 1379  
 DB 1335 CGGATCAGCATGTCGGGGTGAATACGTTCCCGGGTCTTTGTACACACCGCCGCTCACACCA 1394  
 QY 1380 TGGGAGTGGGTTTCCACAGAGCAGGAGTAGTCTTAACCGTAAGGAGGGCGCTTGCACGGTG 1439  
 DB 1395 TGGGAGTGGGTTTCCACAGAGCAGGAGTAGTCTTAACCGTAA-GAGGGCGTTTGCCAGGGG 1453  
 QY 1440 AGATTTCATGACTGG 1453  
 DB 1454 AGATTTCATGACTGG 1467

## RESULT 8

ABR02418  
 ID ABR02418 standard; DNA; 1458 BP.

XX ABA02418;

DT 29-AUG-2003 (revised)

DT 04-MAR-2002 (first entry)

XX Type B ammonia-oxidising bacterium 16S rRNA gene sequence, R3clones5.

XX Type B; ammonia-oxidising bacterium; AOB; nitrite; 16S rRNA gene;

KW ribosomal RNA; aquarium; aquaculture; waste water treatment;

KW bioremediation; ds.

XX Nitrosomonadales.

OS WO200190312-A1.

XX 29-NOV-2001.

XX 17-MAY-2001; 2001WO-US016265.

XX 19-MAY-2000; 2000US-00573684.

XX (AQUA-) AQUARIA INC.

XX Hovanec TA, Burrell PC;

XX WPI; 2002-075367/10.

PT New bacteria capable of oxidizing ammonia to nitrite, for preventing or  
 PT alleviating the accumulation of ammonia in fresh water aquaria, seawater  
 PT aquaria and waste water.

XX Claim 2; Page 7; 62pp; English.

XX The invention relates to 4 novel types of ammonia-oxidising bacteria

CC (AOB) found in freshwater aquaria. The bacteria are able to oxidise

CC ammonia to nitrite and are members of the ammonia-oxidising bacteria

CC family of the beta subdivision of Proteobacteria. The 4 types of bacteria

CC can be distinguished on the basis of their 16S rRNA (ribosomal RNA) gene

CC sequences (ABR02416-ABR02419), and are classified as AOB type A (e.g.,

CC R7clone140), type A1 (e.g., R7clone187), type B (e.g., R3clones5) and type  
 CC C (e.g., R3clone47). The invention also encompasses isolated 16S rRNA  
 CC gene sequences of the ammonia-oxidising bacteria of the invention,  
 CC oligonucleotide probes and primers for the detection of these bacteria,  
 CC and compositions comprising the bacteria. The bacteria of the invention  
 CC are useful in biological filters for reducing ammonia accumulation in  
 CC both freshwater and seawater aquaria. They may also be used in waste  
 CC water treatment and in bioremediation processes to reduce the level of  
 CC pollution caused by ammonia. The present sequence represents R3clone5, a  
 CC 16S rRNA gene sequence from the type B ammonia-oxidising bacterium of the  
 CC invention. (Updated on 29-AUG-2003 to standardise OS field)  
 XX

SQ Sequence 1458 BP; 368 A; 342 C; 466 G; 282 T; 0 U; 0 Other;

Query Match 88.4%; Score 1287.6; DB 6; Length 1458;

Best Local Similarity 93.6%; Pred. No. 0;

Matches 1366; Conservative 0; Mismatches 89; Indels 5; Gaps 2;

QY 1 ATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAACGCCAGCACGCGATGCTTGCAT 60  
 DB 1 ATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAACGCCAGCACGCGCGCAACC-- 58  
 QY 61 CTGTGGCGAGTGGCGGACGGGTGAGTAATGCATCGGAACGTATCCAGAAGAGGGGGTA 120  
 DB 59 CTGTGGCGAGTGGCGGAAACGGGTGAGTAATACATCGGAACGTATCTTCAGGGGGGATA 118  
 QY 121 ACGCATCGAAGATGTGCTAATACCGCATATCTCTAAGGAGGAAGCAGGGGATCGAAA 180  
 DB 119 ACGCACCGAAGGTGTCTAATACCGCATATCTCTAAGGAGGAAGCAGGGGATCGCAA 178  
 QY 181 GACCTTGGCTTTTGGAGCGCGCGATGCTGTAGTAGTCTGTGGTGGGTAAGGGCTTAC 240  
 DB 179 GACCTTGGCTTTTGGAGCGCGCGATGCTGTAGTAGTCTGTGGTGGGTAAGGGCTTAC 238  
 QY 241 CAAGCGCAGCATCAGTAGTGTGTGAGAGGACGACCACTGAGCACTGGGACTGAGACAG 300  
 DB 239 CAAGCGCAGCATCAGTAGTGTGTGAGAGGACGACCACTGAGCACTGGGACTGAGACAG 298  
 QY 301 GCCGAGACTCTACGGGAGGCGAGTGGGAGATTTTGGACAAATGGGCGCAAGCTGATC 360  
 DB 299 GCCGAGACTCTCTACGGGAGGCGAGTGGGAGATTTTGGACAAATGGGCGCAAGCTGATC 358  
 QY 361 CAGCAATCCCGCTGAGTGAGAGAGGCGCTTCGGGTGTGTAAGCTCTTTCAGTCCGAGAAC 420  
 DB 359 CAGCAATCCCGCTGAGTGAGAGAGGCGCTTCGGGTGTGTAAGCTCTTTCAGCAGGACGA 418  
 QY 421 AAAGGTTACGGTAAATATCGTGAATCATGACGCTATCGACAGAGAAGCACAACGGCTAAC 480  
 DB 419 AAAGGTTACGGTAAATATCGTGAATCATGACGCTATCGACAGAGAAGCACAACGGCTAAC 478  
 QY 481 TACGTGCCAGCAGCGCGGTAAATAGTAGGTCGACGCTTAATCGGAATTAATCGGGCT 540  
 DB 479 TACGTGCCAGCAGCGCGGTAAATAGTAGGTCGACGCTTAATCGGAATTAATCGGGCT 538  
 QY 541 AAAGGTTGCCAGCGCGCTTTTGAAGTCAGATGTGAATCCCGGCTTAACTCGGGAAT 600  
 DB 539 AAAGGTTGCCAGCGCGCTTTTGAAGTCAGATGTGAATCCCGGCTTAACTCGGGAAT 598  
 QY 601 TCGGTTTCAAACTACAAGGCTAGAGTGTGGCAGAGGGAGGTGGAATTCATGTAGTAGAG 660  
 DB 599 TCGGTTTCAAACTACAAGGCTAGAGTGTGGCAGAGGGAGGTGGAATTCATGTAGTAGAG 658  
 QY 661 TGAATGCTAGAGTATGGAAGACATCGATGGCGAGGAGCGCTCTCTGGGTTAACTACT 720  
 DB 659 TGAATGCTAGAGTATGGAAGACATCGATGGCGAGGAGCGCTCTCTGGGTTAACTACT 718  
 QY 721 GACGCTCATGCAAGAAAGCGTGGGAGCAAAACAGGATTAGATACCTGTGTAGTCCACGCC 780  
 DB 719 GACGCTCATGCAAGAAAGCGTGGGAGCAAAACAGGATTAGATACCTGTGTAGTCCACGCC 778  
 QY 781 CTAAACGATGTCACATAGTGTGTGGGCTTATTAGGCTTGGTAAACGAGCTAACCGTGA 840  
 DB 779 CTAAACGATGTCACATAGTGTGTGGGCTTATTAGGCTTGGTAAACGAGCTAACCGTGA 838







QY 721 GACGCTCATGCGAAGCGTGGGAGCAAA CAGGATTAGATACCTCGTAGTCCACGCC 780  
 Db 719 GACGCTCAGGCGCAAGCGTGGGAGCAAA CAGGATTAGATACCTCGTAGTCCACGCC 778  
 QY 781 CTAAACGATGTCACTAGTTGTTGGCCCTTATTAGGCTTGGTAACGAAGCTAACGGTGA 840  
 Db 779 CTAAACGATGTCACTAGTTGTTGGCCCTTATTAGGCTTGGTAACGAAGCTAACGGTGA 838  
 QY 841 AGTTGACCCGCTGGGAGTAGTCCGATCGCAAGATTAAAACTCAAAGGAATTGACGGGACCC 900  
 Db 839 AGTTGGCCGCTGGGAGTAGTCCGATCGCAAGATTAAAACTCAAAGGAATTGACGGGACCC 898  
 QY 901 GCACAGCGGTGATTATGTTGATTAATTCGATGCAACGGCAAAACCTTACTACCTT 960  
 Db 899 GCACAGCGGTGATTATGTTGATTAATTCGATGCAACGGCAAAACCTTACTACCTT 958  
 QY 961 GACATGTAGCGAATTTCTAGAGATAGATTAGTGC---TTCGGGAACGCTAACACAGGTG 1017  
 Db 959 GACATGTAGCGAAGCCCGGAGAGGTGGTGTGCCGAAGAGGAGCGGTAAACAGGTG 1018  
 QY 1018 CTGCAATGCTGCTGCTGAGTGTGCTGAGATGTTGGGTAAAGTCCCGCAACGAGCGCA 1077  
 Db 1019 CTGCAATGCTGCTGCTGAGTGTGCTGAGATGTTGGGTAAAGTCCCGCAACGAGCGCA 1078  
 QY 1078 ACCTTGTCAATTAATTCGATCAATTTGGTTGGCACTTTAATGAGACTCCCGTGACAAA 1137  
 Db 1079 ACCTTGTCAATTAATTCGATCAATTTGGTTGGCACTTTAATGAGACTCCCGTGACAAA 1138  
 QY 1138 CCGGAGGAGGTGGGATGACGCTCAAGTCTCATGSCCTTATGGTAGGGCTTCACAG 1197  
 Db 1139 CCGGAGGAGGTGGGATGACGCTCAAGTCTCATGSCCTTATGGTAGGGCTTCACAG 1198  
 QY 1198 TAATACAAATGGGCGTACAGAGGTTGCCAACCCGCGAGGGGAGCTAATCTCAGAAAGC 1257  
 Db 1199 TAATACAAATGGGCGTACAGAGGTTGCCAACCCGCGAGGGGAGCTAATCTCAGAAAGC 1258  
 QY 1258 GCGTGTAGTCCGATCGGAGTGTGCAACTCGACTCGGTGAAGTGGGAATCGTAGTAAT 1317  
 Db 1259 GCGTGTAGTCCGATCGGAGTGTGCAACTCGACTCGGTGAAGTGGGAATCGTAGTAAT 1318  
 QY 1318 CCGGATCAGCATGTCCGCTGAATACGTTCCCGGTCTTGATACACCCCGCTGCACAC 1377  
 Db 1319 CCGGATCAGCATGTCCGCTGAATACGTTCCCGGTCTTGATACACCCCGCTGCACAC 1378  
 QY 1378 CATGGAGTGGGTTTCCACAGAGCAGGTAGTCTAACCCGTAAGGAGGGCGCTTGCCACGG 1437  
 Db 1379 CATGGAGTGGGTTTCCACAGAGCAGGTAGTCTAACCCGTAAGGAGGGCGCTTGCCACGG 1438  
 QY 1438 TGAGATTCAATGCTGGGTG 1457  
 Db 1439 TGAGATTCAATGCTGGGTG 1458

RESULT 10

ABA02419

ID ABA02419 standard; DNA; 1460 BP.

XX ABA02419;

AC ABA02419;

XX 29-AUG-2003 (revised)

DT 04-MAR-2002 (first entry)

XX Type C ammonia-oxidising bacterium 16S rRNA gene sequence, R3clone47.

DE Type C; ammonia-oxidising bacterium; AOB; nitrite; 16S rRNA gene;

XX ribosomal RNA; aquarium; aquaculture; waste water treatment;

KW bioremediation; ds.

XX Nitrosomonadales.

OS WO200190312-A1.

XX

PN

XX

XX

XX

XX

PD 29-NOV-2001.  
 XX 17-MAY-2001; 2001WO-US016265.  
 XX 19-MAY-2000; 2000US-00573684.  
 XX (AQUA-) AQUARIA INC.  
 XX Hovanec TA, Burrell PC;  
 XX WPI; 2002-075367/10.  
 XX New bacteria capable of oxidizing ammonia to nitrite, for preventing or  
 PT alleviating the accumulation of ammonia in fresh water aquaria, seawater  
 PT aquaria and waste water.  
 XX Claim 2; Page 8; 62pp; English.  
 PS The invention relates to 4 novel types of ammonia-oxidising bacteria  
 CC (AOB) found in freshwater aquaria. The bacteria are able to oxidise  
 CC ammonia to nitrite and are members of the ammonia-oxidising bacteria  
 CC family of the beta subdivision of Proteobacteria. The 4 types of bacteria  
 CC can be distinguished on the basis of their 16S rRNA (ribosomal RNA) gene  
 CC sequences (ABA02416-ABA02419), and are classified as AOB type A (e.g.,  
 CC R7clone140), type A1 (e.g., R7clone187), type B (e.g., R3clone5) and type  
 CC C (e.g., R3clone47). The invention also encompasses isolated 16S rRNA  
 CC gene sequences of the ammonia-oxidising bacteria of the invention,  
 CC oligonucleotide probes and primers for the detection of these bacteria,  
 CC and compositions comprising the bacteria. The bacteria of the invention  
 CC are useful in biological filters for reducing ammonia accumulation in  
 CC both freshwater and seawater aquaria. They may also be used in waste  
 CC water treatment and in bioremediation processes to reduce the level of  
 CC pollution caused by ammonia. The present sequence represents R3clone47, a  
 CC 16S rRNA gene sequence from the type C ammonia-oxidising bacterium of the  
 CC invention. (Updated on 29-AUG-2003 to standardise OS field)  
 XX SQ Sequence 1460 BP; 388 A; 316 C; 454 G; 302 T; 0 U; 0 Other;

Query Match 84.4%; Score 1230.2; DB 6; Length 1460;  
 Best Local Similarity 92.3%; Pred. No. 0;  
 Matches 1351; Conservative 0; Mismatches 103; Indels 9; Gaps 5;

QY 1 ATTTGAACCTGCGCATGCTTTACACATGCAAGTCGAAACGCGCAGCAGCGATGCTTGCAT 60  
 Db 1 ATTTGAACCTGCGCATGCTTTACACATGCAAGTCGAAACGCGCAGCAGCGATGCTTGCAT 58  
 QY 61 CTGTTGGCGAGTGGCGGAGTGAATGATCGATCGGACGATTCAGAGAGGGGGTGA 120  
 Db 59 CTGCGCGGAGTGGCGGAGTGAATGATCGATCGGACGATGCTTAAAGTGGGGAATA 118  
 QY 121 ACGCATCGAAAGATGTGCTAATACCGCATATCTTAAGGAGGAAGCAGGGGATCGAA 180  
 Db 119 ACGCATCGAAAGATGTGCTAATACCGCATATCTTAAGGAGGAAGCAGGGGATCGCA 177  
 QY 181 GACCTTGGCTTTTGGAGCGCGCATGCTGATTAGTGTGTTGGGTAAAGGCTTAC 240  
 Db 178 GACCTTGGCTTTAAGGAGCGCGCATGCTGATTAGTGTGTTGGGTAAAGGCTTAC 237  
 QY 241 CAAGGCGACGATCAGTAGTGTGCTGAGAGGACGACCGACCACTGGGACTGAGACAG 300  
 Db 238 CAAGGCGACGATCAGTAGTGTGCTGAGAGGACGACCGACCACTGGGACTGAGACAG 297  
 QY 301 GCCCAGACTCTTACCGGAGGCGAGTGGGGAATTTTGGCAATGGGCGCAAGCCTGATC 360  
 Db 298 GCCCAGACTCTTACCGGAGGCGAGTGGGGAATTTTGGCAATGGGCGCAAGCCTGATC 357  
 QY 361 CAGCAATCCCGCTCAGTGAAGAGGCTTCCGGTGTAAAGCTCTTTCACTCGAGAAAG 420  
 Db 358 CAGCAATCCCGCTCAGTGAAGAGGCTTCCGGTGTAAAGCTCTTTCACTCGAGAAAG 417  
 QY 421 AAAGGTTACGGTAAATATCGTACTCATGAGCGGTATCGACAGAAAGACCGGCTAAC 480  
 Db 418 AAAGGTTACGGTAAATATCGTACTCATGAGCGGTATCGACAGAAAGACCGGCTAAC 477







Db 76 CTGGTGGCGAGTGGCGAAGCGGGTGAATGATCGAAGCTACCCAGTAGTGGGGGATA 135  
Qy 121 AGCATCGAAGATGTGCTTAATACCGCATATATCTTAAGAGGAAAGACGAGGGGATCGAAA 180  
Db 136 GCGCGGCGAAGACCGGATTAATACCGCATATTTCTTGAGGAGAAAGACGCGGGACCTTCG 195  
Qy 181 GACCTTGGCCTTTTGGAGCGCGGATGTCTGATTAGCTAGTTGGTGGGCTAAAGGCGCTAC 240  
Db 196 GCGCTCGCCTACTGGAGCGGCTGATGTGCGATTAGTTGGTGGGCTAAAGGCGCTAC 255  
Qy 241 CAAGGCGACGATCAGTAGTTGGTCTGAGAGGACGACCGACACACCTGGGACTGAGACAG 300  
Db 256 CAAGGCGACGATCCGTAGTGTCTGAGAGGATGATCAGCCACACTGGGACTGAGACAG 315  
Qy 301 GCGCAGACTCTACGGAGGACGACGATGGGGAATTTTGGACAAATGGGCGCAAGCTGATC 360  
Db 316 GCGCAGACTCTACGGAGGACGACGATGGGGAATTTTGGACAAATGGGCGCAAGCTGATC 375  
Qy 361 CAGCAATGCGGTGAGTCAAGAGGCGCTTCGGTGTAAAGCTCTTTCAGTTCGAGAGA 420  
Db 376 CAGCAATGCGGTGAGTCAAGAGGCGCTTCGGTGTAAAGCTCTTTCAGTTCGAGAGA 435  
Qy 421 AAAGGTTACGGTAAATAATCGTGACTCATGACGGTATCGACAGAGAAAGACCGGCTAAC 480  
Db 436 AATCATGCGCCCCGATACCGGCGGTGATGACGGTACCATCAGAGAGACACCGGCTAAC 495  
Qy 481 TAGTGCAGACGACCGCGGTAAATCGTAGGGTCAAGCGTTAATCGGAATTAATCGGGGT 540  
Db 496 TAGTGCAGACGACCGCGGTAAATCGTAGGGTCAAGCGTTAATCGGAATTAATCGGGGT 555  
Qy 541 AAAGGTTGCGAGGCGGTTCGTAGTCAAGTGTGAATCCCGGCGCTTAACCTCGGAAT 600  
Db 556 AAAGGTTGCGAGGCGGTTCGTAGTCAAGTGTGAATCCCGGCGCTTAACCTCGGAAT 615  
Qy 601 TCGCTTTGAAATACAGGCTAGAGTGTGCGAGAGGAGTGGAAATTCATGTGTAGCAG 660  
Db 616 TCGCTTTGAAATACAGGCTAGAGTGTGCGAGAGGAGTGGAAATTCATGTGTAGCAG 675  
Qy 661 TGAATGCTAGAGATATGGAAGAACATCGATGGCGAAGGCGCTCTGTGGTTAACTACT 720  
Db 676 TGAATGCTAGAGATATGGAAGAACATCGATGGCGAAGGCGCTCTGTGGTTAACTACT 735  
Qy 721 GACGCTCATGCAAGAGCGTGGGAGCAACAGGATAGATACCTGTGTAGTCCACGCC 780  
Db 736 GACGCTCATGCAAGAGCGTGGGAGCAACAGGATAGATACCTGTGTAGTCCACGCC 795  
Qy 781 TAAACGATGTCAACTAGTTGTT--GGGCTTTATTAGGCTTGGTAAACGAGCTAACCGGT 838  
Db 796 CTAAACGATGTCAACTAGTTGTTTCGAGAGGAACTTTCTGGGTAAACGAGCTAACCGGT 855  
Qy 839 GAAGTTGACCGCTGGGAGTACGCTGCGAAGATTAAACTCAAGGAATTGACCGGGAC 898  
Db 856 GAAGTTGACCGCTGGGAGTACGCTGCGAAGATTAAACTCAAGGAATTGACCGGGAC 915  
Qy 899 CGCACAAGCGGTGATATGTGGATTAAATTCGATGCAACGCGAAGAACTTACCTACCC 958  
Db 916 CGCACAAGCGGTGATATGTGGATTAAATTCGATGCAACGCGAAGAACTTACCTACCC 975  
Qy 959 TTGACATGTAGCGAATTTCTAGAGATAGATTAGTG-CTTCGGGAAACGCTTAACACAGGTG 1017  
Db 976 TTGACATGTAGCGAATTTCTAGAGATAGATTAGTG-CTTCGGGAAACGCTTAACACAGGTG 1035  
Qy 1018 CTGATGCTGTGCTGACGCTGTGCTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCA 1077  
Db 1036 CTGATGCTGTGCTGACGCTGTGCTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCA 1095  
Qy 1078 ACCCTTGTCATTAATGTCATTTGTTGGGCACTTTAATGACATGCGCGGTGACAAA 1137  
Db 1096 ACCCTTGTCATTAATGTCATTTGTTGGGCACTTTAATGACATGCGCGGTGACAAA 1155  
Qy 1138 CCGAGGAGGTTGGGATGACGTCAGTCCCTCATGGCCCTTATGGGTAGGGCTTCACACG 1197  
Db 1156 CCGAGGAGGTTGGGATGACGTCAGTCCCTCATGGCCCTTATGGGTAGGGCTTCACACG 1215

Qy 1198 TAATCAATATGGCGCTACAGAGGGTTGCCAACCCCGAGGGGAGCTAATCTCAGAAAGC 1257  
Db 1216 TCATCAATATGGTCCGTACAGAGGGTTGCCAAGCCCGAGGTGGAGCAATCCAGAAAGC 1275  
Qy 1258 GCGTCTAGTCCGATCGAGTCTCAACTCGACTCCGTGAAGTCGGAATCGCTAGTAAT 1317  
Db 1276 CGATCGTATCCGATTCGAGTCTCAACTCGACTCCATGAAGTCGGAATCGCTAGTAAT 1335  
Qy 1318 CCGGATCAGCATGTTCGCGGTGAATACGTTCCCGGCTCTTGTACACACCGCCCGTCACAC 1377  
Db 1336 CCGGATCAGCATGTTCGCGGTGAATACGTTCCCGGCTCTTGTACACACCGCCCGTCACAC 1395  
Qy 1378 CATGGAGTGGTTTACACAGAGCAGGTAGTCTTAACCGTAAGAGGGGCTTGCACCG 1437  
Db 1396 CATGGAGTGGTTTACACAGAGTAGTCTTAACCTTCGGGAGGGGCTTACACCG 1455  
Qy 1438 TGAGATTTCATGACTGGGGTG 1457  
Db 1456 TGAGATTTCATGACTGGGGTG 1475

## RESULT 14

AAC86026

ID AAC86026 standard; cDNA; 1460 BP.

XX AAC86026;

XX 06-AUG-2003 (revised)

DT 29-AUG-2001 (first entry)

XX 16S rDNA, SBRA220.

XX 16S rDNA; polyphosphate accumulating organism; PAO; probe; primer;  
detection; phosphorus; waste water; sludge; ss.

XX Unidentified.

XX W0200146459-A1.

XX 28-JUN-2001.

XX 28-DEC-2000; 2000WO-AU001611.

XX 23-DEC-1999; 99AU-00004867.

XX (CRCW-) CRC WASTE MANAGEMENT &amp; POLLUTION CONTROL.

XX Hugenholtz P, Crocetti GR, Tyson GW, Blackall LL;

XX WPI; 2001-408656/43.

XX Novel oligonucleotide probe or primer useful for detecting polyphosphate  
accumulating organism in a sample, comprises a sequence that is unique to  
16S rDNA of polyphosphate accumulating organisms.

XX Claim 4; Fig 3; 54pp; English.

XX The sequences given in AAC86021-30 represent 16S rDNA sequences from  
polyphosphate accumulating organisms (PAOs). Sequences which are unique  
to these 16S rDNA sequences are used to create a probe or primer for  
detecting the relevant organisms. The primer/probe sequences are useful  
for detecting PAO cells in a sample, by treating cells with the primer/probe  
to fix cellular contents, contacting fixed cells with the primer/probe which  
is labelled with a radiolabel, a reporter group or a hapten, within the  
conditions which allow the probe to hybridize with 16S rDNA within the  
fixed cell, removing unhybridized probe from the fixed cells, and  
detecting the labeled probe-RNA hybrid by fluorescence in situ  
hybridization. The primer/probe sequences are useful for identifying PAOs  
that are capable of biologically removing phosphorus from waste water.  
XX Rapid assessment of the presence of a number of PAOs in a waste water  
sample, can be done using the primer/probe sequences. They allow quick  
and convenient assessment of whether a sludge or waste water sample

CC includes PAOs and allows quantitation of PAO cells in samples. (Updated  
 CC on 06-AUG-2003 to correct OS field.)

SQ Sequence 1460 BP; 359 A; 338 C; 475 G; 288 T; 0 U; 0 Other;  
 Query Match 81.9%; Score 1194; DB 4; Length 1460;  
 Best Local Similarity 89.9%; Pred. No. 0;  
 Matches 1315; Conservative 0; Mismatches 140; Indels 7; Gaps 3;  
 QY 1 ATTGAACGCTGGCGGATGCTTTACATCATCAAGTCGAACGGCAGCAGCGATGCTTGCAT 60  
 DB 1 ATTAAACGCTGGCGGATGCTTTACATCATCAAGTCGAACGGCAGCAGCGGCGCAACC-- 58  
 QY 61 CTGGTGGCAGTGGCGGAGCGGGTGAATGATCGATCGGAACGATCCAGAGAGGGGGTA 120  
 DB 59 CTGGTGGCAGTGGCGGAGCGGGTGAATGATCGGAACGATCCAGAGAGGGGGTA 118  
 QY 121 AGCCATCGAAAGATGCTTAATACCCCATATATCTTAAGAGAGAAAGCAGGGGATCGAAA 180  
 DB 119 AGCAGGAAAGCTACGCTTAATACCCCATATATCTTAAGAGAGAAAGCAGGGGATCGAAA 178  
 QY 181 GACCTTGGCCTTTGGAGCGGCGATGCTCTGATTAAGTCTAGTTGGTGGGTAAAGCCTAC 240  
 DB 179 GACCTTGGCCTTTGGAGCGGCGATGCTCTGATTAAGTCTAGTTGGTGGGTAAAGCCTAC 238  
 QY 241 CAAAGGAGATCAGTAGTTGGTCTGAGAGAGCAGCAGCCACACTGGGACTGAGACAG 300  
 DB 239 CAAAGGAGATCAGTAGTTGGTCTGAGAGAGCAGCAGCCACACTGGGACTGAGACAG 298  
 QY 301 GCCAGACTCTACGGGAGCGCAGCAGTGGGGATTTGGACAAATGGCGCAGCCTGATC 360  
 DB 299 GCCAGACTCTACGGGAGCGCAGCAGTGGGGATTTGGACAAATGGCGCAGCCTGATC 358  
 QY 361 CAGCAATGCCGCTGAGTCAAGAGCGCTTCGGTGTGTAAGCTCTTTCAAGTCGAAGA 420  
 DB 359 CAGCAATGCCGCTGAGTCAAGAGCGCTTCGGTGTGTAAGCTCTTTCAAGTCGAAGA 418  
 QY 421 AAGGTTAGGTAATTAATCGTCTCATGAGCGTATCGACAGAGAGCAGCGCTAAC 480  
 DB 419 AATGCTTGGGTTAATACCTCGTAGATGAGCGGTACCCGAAATGAAGCAGCGCTAAC 478  
 QY 481 TACGTGCCAGCAGCGCGCTAATACGTAGGGTGAAGCGTTAATCGGAATTAATCGGCGT 540  
 DB 479 TACGTGCCAGCAGCGCGCTAATACGTAGGGTGAAGCGTTAATCGGAATTAATCGGCGT 538  
 QY 541 AAAGGTTGCCAGCGCGCTTTGTAAGTCAGATGTGAATCCCGGCTTAACTGGGAAT 600  
 DB 539 AAAGGTTGCCAGCGCGCTTTGTAAGTCAGATGTGAATCCCGGCTTAACTGGGAAT 598  
 QY 601 TCGCTTTGAACTACAGGCTAGAGTGTGCGAGAGGAGGTGGAATTCATGTGTAGCAG 660  
 DB 599 TCGCTTTGAGACTGCAAGACTGGAGTTTGGCAGAGGGGGTGGAAATCCACGTGTAGCAG 658  
 QY 661 TGAATTCGTAGAGTATGGAAGAACTCATGAGGAGGAGCGCTTCTGGGTAACTACT 720  
 DB 659 TGAATTCGTAGAGTATGGAAGAACTCATGAGGAGGAGCGCTTCTGGGTAACTACT 718  
 QY 721 GACGCTCATGCAAGAGCGTGGGAGCAACAGGATTAATACCTGTGTAGTCCACGCC 780  
 DB 719 GACGCTCATGCAAGAGCGTGGGAGCAACAGGATTAATACCTGTGTAGTCCACGCC 778  
 QY 781 CTAAAGCATGCACTAGTTGTTGG--GCCTTATTAGGCTTGGTAACGAGTACCGGT 838  
 DB 779 CTAAAGCATGCACTAGTTGTTGGAGGTTTAAACCTTTTAGTCCGCTAGTAAACGCT 838  
 QY 839 GAAGTTGACCGCTGGGAGTACGGTGCAGAAATTAATACTCAAGAGGATTCACGGGAC 898  
 DB 839 GAAGTTGACCGCTGGGAGTACGGTGCAGAAATTAATACTCAAGAGGATTCACGGGAC 898  
 QY 899 CGGCACAAGCGGTGATTTATGGAATTAATTCGATGCAACGCGAAACCTTACCTACCC 958  
 DB 899 CGGCACAAGCGGTGATTTATGGAATTAATTCGATGCAACGCGAAACCTTACCTACCC 958

RESULT 15

ABL40355  
 ID ABL40355 standard; DNA; 1464 BP.  
 AC ABL40355;  
 XX AC ABL40355;  
 XX AC ABL40355;  
 DT 01-JUL-2002 (first entry)  
 XX  
 DE Sequence related to an oligonucleotide for the detection of Azoarcus sp.  
 XX Selenic acid; MA-23; ds.  
 XX Azoarcus sp.  
 XX JP2001346584-A.  
 XX 18-DEC-2001.  
 XX 07-JUN-2000; 2000JP-00170641.  
 XX 07-JUN-2000; 2000JP-00170641.  
 XX (MITO) MITSUBISHI JUKOGYO KK.  
 XX WPI; 2002-199319/26.  
 XX Novel oligonucleotide useful for specific detection of a selenic acid  
 PT reducing microbe.  
 XX Example 1; Page 6; 7pp; Japanese.  
 CC The invention relates to an oligonucleotide that may be used for  
 CC detecting Azoarcus sp. strain MA-23, a selenic acid reducing microbe. The  
 CC current sequence represents a sequence related to an oligonucleotide for  
 CC the detection of Azoarcus sp

QY 959 TTGCATCTAGCGATTTTCTAGAGATAGATTAGTGTCT---TCGGGAAGCTTAACACAGG 1015  
 DB 959 TTGCATCTAGCGATTTTCTAGAGATAGATTAGTGTCT---TCGGGAAGCTTAACACAGG 1018  
 QY 1016 TGCTGCATGGCTGTCTGTCAGCTCGTGTGATGATGTTGGGTAAAGTCCCGCAACGAGCG 1075  
 DB 1019 TGCTGCATGGCTGTCTGTCAGCTCGTGTGATGATGTTGGGTAAAGTCCCGCAACGAGCG 1078  
 QY 1076 CAACCTTGTCTAATTAATGTCATCTTTGGTGGGACCTTTAATGAGACTGCGGTGACA 1135  
 DB 1079 CAACCTTGTCTAATTAATGTCATCTTTGGTGGGACCTTTAATGAGACTGCGGTGACA 1138  
 QY 1136 AACCGGAGAGGTGGGATGAGCTCAAGTCTCTATGCGCTTATGGGTAGGGCTTCA 1195  
 DB 1139 AACCGGAGAGGTGGGATGAGCTCAAGTCTCTATGCGCTTATGGGTAGGGCTTCA 1198  
 QY 1196 CGTAATCAATGGCGCTGACAGAGGGTTCACACCCGCGAGGGGAGCTTAATCTCAGAAA 1255  
 DB 1199 CGTCATCAATGGTCCGTCAGAGGGTTCACACCCGCGAGGGGAGCTTAATCTCAGAAA 1258  
 QY 1256 GCGGCTCTAGTCCGATCGGAGTCTGCAACTCGACTCGTGAAGTCCGAAATCGCTAGTA 1315  
 DB 1259 GCGGCTCTAGTCCGATCGGAGTCTGCAACTCGACTCGTGAAGTCCGAAATCGCTAGTA 1318  
 QY 1316 ATCGCGATCAGCATGTCGCGTGAATACGTTCCCGGCTTGTACACACCGCCGCTAC 1375  
 DB 1319 ATCGCGATCAGCATGTCGCGTGAATACGTTCCCGGCTTGTACACACCGCCGCTAC 1378  
 QY 1376 ACCATGGAGTGGGTTTCCACGAGAGCAGGAGTAGTCTAAACCGTAAAGAGGGCGCTTGGCCAC 1435  
 DB 1379 ACCATGGAGTGGGTTTCCACGAGAGCAGGAGTAGTCTAAACCGTAAAGAGGGCGCTTGGCCAC 1438  
 QY 1436 GGTGAGATTCATGACTGGGGTG 1457  
 DB 1439 GGCAGGGTTCGTGACTGGGGTG 1460

SQ Sequence 1464 BP; 364 A; 338 C; 470 G; 292 T; 0 U; 0 Other;

Query Match 81.7%; Score 1190.8; DB 6; Length 1464;  
 Best Local Similarity 90.2%; Pred. No. 0;  
 Matches 1320; Conservative 0; Mismatches 137; Indels 7; Gaps 4;

QY 1 ATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAACGGCAGCAGCATGCTTGCAT 60  
 DB 1 ATTGAACGCTGGCGGCATGCTTTACACATGCAAGTCGAACGGCAGCAGCATGCTTGCAT 60

QY 61 CTGGTGGCGAGTGGCGGACGGGTGAGTAATGCAATCGGAACGTAATCCAGAAAGAGGGGGTA 120  
 DB 61 CTGGTGGCGAGTGGCGGACGGGTGAGTAATGCAATCGGAACGTAATCCAGAAAGAGGGGGTA 120

QY 121 ACCGATCGAAGATGTCCTAATACCGCATATCTTAAGCAGGAAACGAGGGGATCGAAA 180  
 DB 121 ACCTAGCGAAGATGTCCTAATACCGCATATCTTAAGCAGGAAACGAGGGGATCGCAA 180

QY 181 GACCTTGCCTTTTGGAGCGCGCATGCTCTGATTTAGTCTGCTGGGTAAAGGCTTAC 240  
 DB 181 GACCTCGCTCTTGGAGCGCGCATGCTCGATTTAGTCTGCTGGGTAAAGGCTTAC 240

QY 241 CAAGGCGACATCAGTATGTTGCTGAGAGGACGACCACTGGGACTGAGACAG 300  
 DB 241 CAAGGCGACATCGTAGCAGGCTGAGAGGATGATCTGCCACACTGGGACTGAGACAG 300

QY 301 GCCCAGACTCTACGGGAGCAGCAGTGGGGATTTTGGCAATGGGCGCAACCTGATC 360  
 DB 301 GCCCAGACTCTACGGGAGCAGCAGTGGGGATTTTGGCAATGGGCGCAACCTGATC 360

QY 361 CAGCAATGCCGCTGAGTGAAGAGGCTTTCGGTGTGTAAGTCTTTCACTGAGAGAA 420  
 DB 361 CAGCAATGCCGCTGAGTGAAGAGGCTTTCGGTGTGTAAGTCTTTTCGGGCGGAGAA 420

QY 421 AAAGGTTACGGTAAATATCTGACTCATCAACGGTATCGACAGAGAACACCGGCTAAC 480  
 DB 421 AATGGCAACGGCTAATATCTGTTGATGACGGTACCCGCTAAGAGCACCGGCTAAC 480

QY 481 TAGCTGCCAGCAGCGCGGTAAATACGTAGGGTGCAGCGTAAATCGGAATTAATCGGGCGT 540  
 DB 481 TAGCTGCCAGCAGCGCGGTAAATACGTAGGGTGCAGCGTAAATCGGAATTAATCGGGCGT 540

QY 541 AAAGGTTGCCAGCGCGCTTTGTAAGTTCAGATGTGAATCCCGGCTTAACTCGGGAA- 599  
 DB 541 AAAGGTTGCCAGCGCGCTTTGTAAGTTCAGATGTGAATCCCGGCTTAACTCGGGAA- 600

QY 600 TTGCGTTTGAACCTACAGGCTAGAGT- GTGGCAGAGGAGGTGGAATTCATGTGTAGC 658  
 DB 601 TGGCGTTTGTGACTGCGAGGCTAGAGTACGGGCGAGAGGGGGTAGAATTCACGTTGTAGC 660

QY 659 AGTGAATGCGTAGAGATATGGAAGAACATCGATGCGGAAGGCGGCTCTGGGTTAAACA 718  
 DB 661 AGTGAATGCGTAGAGATATGGAAGAACATCGATGCGGAAGGCGGCTCTGGGTTAGTA 720

QY 719 CTGACGCTCATGCAAGAGCGTGGGAGCAACAGGATTAGATACCTGGTAGTCCAG 778  
 DB 721 CTGACGCTCATGCAAGAGCGTGGGAGCAACAGGATTAGATACCTGGTAGTCCAG 780

QY 779 CCTTAAACGATGTCAACTAGTGTGTTGG--GCCTTATTAGGCTTTGGTAAACGAACTAACGC 836  
 DB 781 CCTTAAACGATGTCAACTAGTGTGTTGGAGGGTTAAACCTTTTAGTACCGAGCTAACGC 840

QY 837 GTGAAGTTGACCGCTGGGGAGTACGGTGCAGAGATTAAACTCAAAGGAATTGACGGGG 896  
 DB 841 GTGAAGTTGACCGCTGGGGAGTACGGGCGCAAGGTTAAAACTCAAAGGAATTGACGGGG 900

QY 897 ACCCGCACAGCGGTGATTTGTTGATTAATTCGATGCAACCGGAAACCTTACCTAC 956  
 DB 901 ACCCGCACAGCGGTGATTTGTTGATTAATTCGATGCAACCGGAAACCTTACCTAC 960

QY 957 CCTTGACATGTAGCGAAATTTTCTAGAGATAGATTAGTGC--TTCCGGGAAACGCTAACACA 1013  
 DB 961 CCTTGACATGCCAGGAACTTTCCAGAGATGGATTGGTGGCCCGAAAGGAGCCTGGACACA 1020

QY 1014 GGTCTGCAATGGCTGTGCTCAGCTCGTGTGAGATGTTGGTTAAGTCCCGCAACGAG 1073  
 DB 1021 GGTCTGCAATGGCTGTGCTCAGCTCGTGTGAGATGTTGGTTAAGTCCCGCAACGAG 1080

QY 1074 CGCAACCCCTTGTCAATTAATTTGCCATCATTTGGTTGGGCACTTTAAATGAGACTGCCCGTGA 1133  
 DB 1081 CGCAACCCCTTGTCAATTAATTTGCCATCATTTAGTTGGGCACTTTAAATGAGACTGCCCGTGA 1140

QY 1134 CAAACCGGAGGAAGGTGGGATGACGTCAAGTCTCTCATGGCCCTTATGGGTAGGGTTTCA 1193  
 DB 1141 CAAACCGGAGGAAGGTGGGATGACGTCAAGTCTCTCATGGCCCTTATGGGTAGGGTTTCA 1200

QY 1194 CACGTAATACATGGCGGTGAGAGGGTTGCCAACCCCGGAGGGGAGCTAATCTCAGA 1253  
 DB 1201 CACGTCATACATGGGTGCGGTACAGAGGGTTGCCAACCCCGGAGGGGAGCTAATCTCAGA 1260

QY 1254 AAGCGGCTGCTAGTCCGATCGGATCGGATCTGAACTCGACTCCGTTGAAAGTCGGAATCGCTAG 1313  
 DB 1261 AAGCGGATCGTGTAGTCCGATCGGATCGGATCTGCAACTCGACTGCGTGAAGTCGGAATCGCTAG 1320

QY 1314 TAATCGCGGATCAGCATGTGCGGGTGAATACGTTCCCGGGTCTTTGTAACACACCGCCCGTC 1373  
 DB 1321 TAATCGCGGATCAGCATGTGCGGGTGAATACGTTCCCGGGTCTTTGTAACACACCGCCCGTC 1380

QY 1374 ACACCATGGGAGTGGTTTCCACGAGCAGAGTGTCTAACCGTAAAGGAGGGGCGCTTGC 1433  
 DB 1381 ACACCATGGGAGTGGTTTCTACAGAGTGTAGCTTAACCGTAAAGGAGGGGCGATTACC 1440

QY 1434 ACAGGTGAGATTTCATGACTGGGGTG 1457  
 DB 1441 ACAGGTGAGATTTCATGACTGGGGTG 1464

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- 2: /SDSS/p/odata/2/pub/pnua/US06 NEW PUB.seq.\*
- 3: /SDSS/p/odata/2/pub/pnua/US07 NEW PUB.seq.\*
- 4: /SDSS/p/odata/2/pub/pnua/Pct NEW PUB.seq.\*
- 5: /SDSS/p/odata/2/pub/pnua/US09 NEW PUB.seq.\*
- 6: /SDSS/p/odata/2/pub/pnua/US09 NEW PUB.seq1.\*
- 7: /SDSS/p/odata/2/pub/pnua/US10 NEW PUB.seq.\*
- 8: /SDSS/p/odata/2/pub/pnua/US10 NEW PUB.seq1.\*
- 9: /SDSS/p/odata/2/pub/pnua/US10 NEW PUB.seq2.\*
- 10: /SDSS/p/odata/2/pub/pnua/US10 NEW PUB.seq3.\*
- 11: /SDSS/p/odata/2/pub/pnua/US11 NEW PUB.seq.\*
- 12: /SDSS/p/odata/2/pub/pnua/US11 NEW PUB.seq2.\*
- 13: /SDSS/p/odata/2/pub/pnua/US11 NEW PUB.seq3.\*
- 14: /SDSS/p/odata/2/pub/pnua/US11 NEW PUB.seq4.\*
- 15: /SDSS/p/odata/2/pub/pnua/US60 NEW PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score  | Query Match | Length | DB | ID                   | Description       |
|------------|--------|-------------|--------|----|----------------------|-------------------|
| 1          | 1149.2 | 78.9        | 1522   | 11 | US-11-198-242-2      | Sequence 2, Appli |
| 2          | 1142.8 | 78.4        | 1526   | 11 | US-11-198-242-1      | Sequence 1, Appli |
| 3          | 1089.6 | 74.8        | 1405   | 9  | US-10-515-311-5      | Sequence 5, Appli |
| 4          | 1021.8 | 70.1        | 1501   | 9  | US-10-513-639-1      | Sequence 1, Appli |
| 5          | 1021.2 | 70.1        | 1493   | 9  | US-10-831-2864-46683 | Sequence 48683, A |
| 6          | 1020.2 | 70.0        | 1508   | 9  | US-10-831-2864-46685 | Sequence 48685, A |
| 7          | 1019.8 | 70.0        | 1510   | 9  | US-10-831-2864-46680 | Sequence 48680, A |
| 8          | 1019.6 | 70.0        | 1494   | 9  | US-10-831-2864-46681 | Sequence 48681, A |
| 9          | 1018   | 69.9        | 1507   | 9  | US-10-831-2864-46677 | Sequence 48677, A |
| 10         | 1017   | 69.8        | 1508   | 9  | US-10-831-2864-46684 | Sequence 48684, A |
| 11         | 1015.4 | 69.7        | 1510   | 9  | US-10-831-2864-46682 | Sequence 48682, A |
| 12         | 1008.4 | 69.2        | 1530   | 9  | US-10-831-2864-46671 | Sequence 48671, A |
| 13         | 1007.2 | 69.1        | 1492   | 9  | US-10-831-2864-46686 | Sequence 48686, A |
| 14         | 1007.2 | 69.1        | 1519   | 9  | US-10-831-2864-46687 | Sequence 48687, A |
| 15         | 1005.4 | 69.0        | 1495   | 9  | US-10-831-2864-46675 | Sequence 48675, A |
| 16         | 1005.2 | 69.0        | 1494   | 9  | US-10-831-2864-46669 | Sequence 48669, A |
| 17         | 1005.2 | 69.0        | 1504   | 9  | US-10-831-2864-46665 | Sequence 48665, A |
| 18         | 1005.2 | 69.0        | 1514   | 9  | US-10-831-2864-46666 | Sequence 48666, A |

|    |        |      |        |                      |                     |
|----|--------|------|--------|----------------------|---------------------|
| 19 | 1004.8 | 69.0 | 1494.9 | US-10-831-286A-48676 | Sequence 48676, A   |
| 20 | 1003.8 | 66.9 | 1535.5 | US-10-831-286A-48678 | Sequence 48678, A   |
| 21 | 1003.6 | 66.9 | 1501.9 | US-10-831-286A-48670 | Sequence 48670, A   |
| 22 | 1002.8 | 68.6 | 1527.9 | US-10-831-286A-48693 | Sequence 48693, A   |
| 23 | 1000   | 68.8 | 1486.9 | US-10-831-286A-48679 | Sequence 48679, A   |
| 24 | 995.2  | 66.3 | 1542.1 | US-09-941-095-158    | Sequence 158, App   |
| 25 | 995.2  | 66.3 | 1542.1 | US-11-198-946-158    | Sequence 158, App   |
| 26 | 995.2  | 66.3 | 1542.1 | US-11-198-944-158    | Sequence 158, App   |
| 27 | 995.2  | 66.3 | 1542.1 | US-11-198-957-158    | Sequence 158, App   |
| 28 | 990    | 67.9 | 1533.9 | US-10-831-286A-48668 | Sequence 48668, App |
| 29 | 988    | 67.8 | 1418.9 | US-10-831-286A-48691 | Sequence 48691, A   |
| 30 | 988    | 67.8 | 1418.9 | US-10-831-286A-48692 | Sequence 48692, A   |
| 31 | 981.2  | 67.3 | 1436.9 | US-10-831-286A-48667 | Sequence 48667, A   |
| 32 | 979.8  | 67.2 | 1481.9 | US-10-831-286A-48672 | Sequence 48672, A   |
| 33 | 977.8  | 67.1 | 1525.9 | US-10-831-286A-48689 | Sequence 48689, A   |
| 34 | 850.4  | 58.4 | 1485.1 | US-11-055-637-76     | Sequence 76, App    |
| 35 | 848.8  | 58.3 | 1513.1 | US-11-055-637-79     | Sequence 79, App    |
| 36 | 845.8  | 58.1 | 1505.1 | US-11-055-637-80     | Sequence 80, App    |
| 37 | 841.2  | 57.7 | 1509.1 | US-11-373-617-6      | Sequence 6, App1    |
| 38 | 839.6  | 57.6 | 1486.1 | US-11-055-637-69     | Sequence 69, App1   |
| 39 | 838.6  | 57.6 | 1545.1 | US-11-055-637-66     | Sequence 66, App1   |
| 40 | 838.6  | 57.6 | 1587.1 | US-11-373-617-8      | Sequence 8, App1    |
| 41 | 837.2  | 57.5 | 1486.1 | US-11-055-637-71     | Sequence 71, App1   |
| 42 | 837.2  | 57.5 | 1507.1 | US-11-055-637-78     | Sequence 78, App1   |
| 43 | 837    | 57.4 | 3169.8 | US-10-793-626-3356   | Sequence 3356, App  |
| 44 | 837    | 57.4 | 3368.8 | US-10-793-626-3905   | Sequence 3905, App  |
| 45 | 837    | 57.4 | 3657.8 | US-10-793-626-4187   | Sequence 4187, App  |

## ALIGNMENTS

```

RESULT 1
US-11-198-242-2
Sequence 2, Application US/11198242
Publication No. US20060035345A1
GENERAL INFORMATION:
APPLICANT: AJINOMOTO CO., INC.
TITLE OF INVENTION: Processes for the production of beta-amino acids by using acylases
FILE REFERENCE: AB04037
CURRENT APPLICATION NUMBER: US/11/198,242
CURRENT FILING DATE: 2005-08-08
NUMBER OF SEQ. ID NOS: 2
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 1522
TYPE: DNA
ORGANISM: Burkholderia sp.
FEATURE:
NAME/KEY: 16S rDNA
LOCATION: (1)..(1522)
OTHER INFORMATION:
US-11-198-242-2

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|             |        |               |        |              |
|-------------|--------|---------------|--------|--------------|
| Query Match | 78.9%; | Score 1149.2; | DB 11; | Length 1522; |
|-------------|--------|---------------|--------|--------------|

Matches 1287; Conservative 0; Mismatches 163; Indels 10; Gaps 3;

|    |     |   |     |
|----|-----|---|-----|
| QY | 1   | ATTGAAACGCTGGCGGCGCATGCTTTACACATGCAATGCCACGGGACGACCGAATGCTTGCAT | 60  |
| Db | 20  | ATTGAAACGCTGGCGGCGCATGCTTTACACATGCAATGCCACGGGACCGCGGGGCGACCC--  | 77  |
| QY | 61  | CTGGTGGCAGTAGTGGCGGACGGGTGAGTATGCATCGAACGTATCCGAAGAGGGGGGTA     | 120 |
| Db | 78  | CTGGCGGCGAGTGGCGGAACGGGTAGATTAACATCGGAACGTGCTCTGTATGTGGGGATA    | 137 |
| QY | 121 | ACGCATCGAAGATGTCTAATACCGCATATCTCTTAAGAGGAACAGGGGATCGAAA         | 180 |
| Db | 138 | GCCCGGCGAACCAGCAATTAATACCGCATACGCTCTACGGAGGAACAGGGGGGATCTTAA    | 197 |
| QY | 181 | GACCTTGGGCTTTTGAAGCGGCCAATGTCTGATTAGCTAGTGGTGGGGTAAAGGCTTAC     | 240 |
| Db | 198 | GACCTTGCCTACAGAGGCGGGCCATGCGCAATTAGCTAGTGGTGGGGTAAAGGCTTAC      | 257 |

|    |      |  |      |
|----|------|--|------|
| Qy | 241  | CAAGCCACGATCACTAGTATGCTGTGAGAGACACACACGACCACTGGGACTGAGACACG      | 300  |
| Db | 258  | CAAGCGACGATCTGTAGCTGCTGTGAGAGACGACGACCACTGGGACTGAGACACG          | 317  |
| Qy | 301  | GCCGACACTCTTACGGGAGGACGACGAGTGGGAAATTTTGACAAATGGGCGCAAGCTGATC    | 360  |
| Db | 318  | GCCGACACTCTTACGGGAGGACGACGAGTGGGAAATTTTGACAAATGGGCGCAAGCTGATC    | 377  |
| Qy | 361  | CAGCAATGCCCGGTGAGTGAAGAAAGGCTTTGGGGTGTAAAGCTCTTCAATCGAGAA        | 420  |
| Db | 378  | CAGCAATGCCCGGTGAGTGAAGAAAGGCTTTGGGGTGTAAAGCACTTTTGTCCGAAAGA      | 437  |
| Qy | 421  | AAAGGTTACGGTAAATAATTCGTGACTCATGACGCGATGACAGAAAGACACCGGCTAAC      | 480  |
| Db | 438  | AAAGCGCGGTAAATAATTCGCTGTGCGGATGACGATACCGGAAAGAAATAGCACCGGCTAAC   | 497  |
| Qy | 481  | TACGTGCCAGCAGCCGCGGTAAATACGTAAGGTGCACGCTTAATTCGAAATTACTGGCGGT    | 540  |
| Db | 498  | TACGTGCCAGCAGCCGCGGTAAATACGTAGGGGTGCACAGGCTTAATTCGAAATTACTGGCGGT | 557  |
| Qy | 541  | AAAGGGTCCGAGGCGGCTTTGTAAAGTACAGATGTGAAATCCCGGGGCTTAACCTGGGAAT    | 600  |
| Db | 558  | AAAGGTTCCGAGGCGGCTTTGTAAAGTACAGATGTGAAATCCCGGGGCTTAACCTGGGAAC    | 617  |
| Qy | 601  | TGCGTTTGAAACTACAAAGCTAGAGTGTGGCAGAGGAGGTGGAATTCATGTGTGACAG       | 660  |
| Db | 618  | TGCAATTTGTGACTGGCGGGCTAGAAATTAAGCAGAGGGGGGTAAATTCAGTGTGACAG      | 677  |
| Qy | 661  | TGAAATGGGTGAGATATGGAAGAACATTCGATGGGGAAGGACGCTCTTGGGTTAAACAT      | 720  |
| Db | 678  | TGAAATGGGTGAGATATGGAAGAAATACGATGGGGAAGGACGCTCTTGGGCCCAATACT      | 737  |
| Qy | 721  | GACGCTCATGACAGAAACGTGGGAGGACAAACAGGATTAAGATACCTGTAGTCCACGCC      | 780  |
| Db | 738  | GACGCTCATGACAGAAACGTGGGAGGACAAACAGGATTAAGATACCTGTAGTCCACGCC      | 797  |
| Qy | 781  | CTAAACGATGTCACTAGTTGTTGGGCTTATTAGGCTTTGGTACGAAGCTAACGCGTGA       | 840  |
| Db | 798  | CTAAACGATGTCACTAGTTGTTGGGAGTTCACTTCTTAAAGTATGCTAACCGCTGA         | 857  |
| Qy | 841  | AGTTGACCGGCTGGGGAGTAACGCTGCGCAAGATTAATCAACAAAGAAATTGACGGGACCC    | 900  |
| Db | 858  | AGTTGACCGGCTGGGGAGTAACGCTGCGCAAGATTAATCAACAAAGAAATTGACGGGACCC    | 917  |
| Qy | 901  | GCACAAAGCGGTGATTAATGTGATTAATTCGATGCAACGCGCAAAACCTTACCTACCTT      | 960  |
| Db | 918  | GCACAAAGCGGTGATTAATGTGATTAATTCGATGCAACGCGCAAAACCTTACCTACCTT      | 977  |
| Qy | 961  | GACATGTAGCGAAATTTTCTAAGAGATAGATTAATGCTGCGGAAACGCTAACACAGGTG      | 1017 |
| Db | 978  | GACATGTATGAAATCTCTCTGAGAGGTGGGAGTCCCGAAAGGGAGCCATTAACAGAGGTG     | 1037 |
| Qy | 1018 | CTGCATGCTGTGCTCAGCTGCTGCTGAGAGATGTTGGGTTAAAGTCCCGCAACAGCGCA      | 1077 |
| Db | 1038 | CTGCATGCTGTGCTCAGCTGCTGCTGAGAGATGTTGGGTTAAAGTCCCGCAACAGCGCA      | 1097 |
| Qy | 1078 | ACCCTGTTCATTAATTCGCATCATTTGGTGGGCACTTTATGAGACTGCGCGGTACAA        | 1137 |
| Db | 1098 | ACCCTGTTCCTTAAGTTGCTTAC-----GCAAAGGCACTCTAGGGAACATCGCGGTACAA     | 1152 |
| Qy | 1138 | CCGAGGAAGGTGGGGATGACGTCAAGTCCCTATAGGCCCTTAATGGGTAGGGCTTACACG     | 1197 |
| Db | 1153 | CCGAGGAAGGTGGGGATGACGTCAAGTCCCTATAGGCCCTTAATGGGTAGGGCTTACACG     | 1212 |
| Qy | 1198 | TAAATCAATGGGCGCTACAGAGGTTGCCAACCCGCGAGGGGAGACTAATTCAGAAAGC       | 1257 |
| Db | 1213 | TCAATCAATGGGCGGAAACAGAGGGTCCGCAACCCGCGAGGGGAGCAATCCAGAAAGC       | 1272 |
| Qy | 1258 | GCGTGTATGCTCCGATTCGGAATCTGCAACTGCACTCCGTTGAAGTGGGAATGCTATGAT     | 1312 |
| Db | 1273 | GCGTGTATGCTCCGATTCGCAACTCTGTCAATCTGCAATGCGTGAAGCTGGAATCGCTATGAT  | 1333 |

|    | 1317  | 1318 | 1333 | 1378   | 1393 | 1438                  | 1453 |
|----|---|------|------|--|------|-----------------------|------|
| QY | CGCGGATCAGACAGTCCGCGGTGAAATAGCTCCCGGGCTTGTAACAACCGCGCGTCAAC |      |      |  |      |                       |      |
| Db | CGCGGATCAGACAGTCCGCGGTGAAATAGCTCCCGGGCTTGTAACAACCGCGCGTCAAC |      |      |  |      |                       |      |
| QY |   |      |      | CATGGAGTGGGGTTTCCAGAAAGCAGTAGTCTAACCGTAAGAGAGGAGCGCTTGCCACGG |      |                       |      |
| Db |   |      |      | CATGGAGTGGGGTTTCCAGAAAGTGGCTAGTCTAACCGCAAGAGGACGGTACCAACGG   |      |                       |      |
| QY |   |      |      |  |      | TGAGATTCACTAGCTGGGGTG | 1457 |
| Db |   |      |      |  |      | TGAGATTCACTAGCTGGGGTG | 1472 |

```

RESULT 2
US-11-198-242-1
; Sequence 1, Application US/11198242
; Publication No. US20060035345A1
; GENERAL INFORMATION:
; APPLICANT: AJINOMOTO CO., INC.
; TITLE OF INVENTION: Process for the production of beta-amino acids by using acylases
; FILE REFERENCE: ABO4037
; CURRENT APPLICATION NUMBER: US/11/198,242
; CURRENT FILING DATE: 2005-08-08
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1
; LENGTH: 1526
; TYPE: DNA
; ORGANISM: Varilovorax sp.
; FEATURE:
; NAME/KEY: 16S rDNA
; LOCATION: (1)..(1526)
; OTHER INFORMATION:
US-11-198-242-1

```

| Query Match  | Similarity   | 78.4%   | Score 1142.8   | DB 11    | Length 1526 |
|--------------|--------------|---|----------------|----------|-------------|
| Best Local   | 87.8%        | Pred. No. 0   |                |          |             |
| Matches 1282 | Conservative | 0   | Mismatches 172 | Indels 6 | Gaps 3      |
| QY           | 1            | ATTGACGCTGGCGCAGTGCCTTTACACATGCAGTTCGACCGCAGCAGCAGATGCTTGAT     | 60             |          |             |
| Db           | 20           | ATTGAAGCGCTGGCGGCATGCCCTTACATCATGCAATCGAACGGCAGCGCCGGAGCAATC--  | 77             |          |             |
| QY           | 61           | CTGCTGGCGAGTGGCGGACGGGTGATGTAATGATCCGAACGTATCCGAAGAGGGGGGTA     | 120            |          |             |
| Db           | 78           | CTGGCGGGAGATGGCGGAACGGGTGATGTAATACATCGGAACGTGCCCAATCGTGGGGGATA  | 137            |          |             |
| QY           | 121          | ACGCATCGAAGATGTGCTAATAACGGATATTACTCTAAGAGGAGAAACAGGGGATCGAAA    | 180            |          |             |
| Db           | 138          | ACGCAGCGAAGCTGTGCTAATACCGATACGATCTACGATGGAAGAACAGGGGATTCGCA     | 197            |          |             |
| QY           | 181          | GACCTTGGCTTTTGGAGCGGCGCATGTCTTGATTAGCTAAGTTGGTGGGTTAAAGCCTTAC   | 240            |          |             |
| Db           | 198          | GACCTTGGCGCAATAGGAGCGGCGCATAGGACAGATTAGGTGGTGGATGATTAAGGCTCAC   | 257            |          |             |
| QY           | 241          | CAAGGCCACGATCGATGATGTGTTGAGAGGACGACCAAGCCACACTGAGACACG          | 300            |          |             |
| Db           | 258          | CAAGCTTGCATCTGTAGCTGTGAGAGGACGACCAAGCCACACTGGGACTGAGACACG       | 317            |          |             |
| QY           | 301          | GCCGAGACTCTTACCGGAGGCGCAGCAGTGGGGAAATTTTGAACAATGGGCGCAAGCCTGATC | 360            |          |             |
| Db           | 318          | GCCGAGACTCTTACGGGAGGCGCAGCAGTGGGGAAATTTTGAACAATGGGCGCAAGCCTGATC | 377            |          |             |
| QY           | 361          | CAGCAATGCCGCGTGAAGTGAAGAAAGGCTTCGGGTTGTAAAGCTCTTCAATCGAAGAA     | 420            |          |             |
| Db           | 378          | CAGCCATGCCCGCGCAGATGAAGGGCTTCGGGTTGTAAAGCTCTTGTACGAAACGA        | 437            |          |             |
| QY           | 421          | AAAGTTACGGTAATATCGTGAATCATGACGGTATCGACAGAGAAGACACCGGCTAAC       | 480            |          |             |
| Db           | 438          | AAAGGCTCTTTCTAATTAAGAGGGCTAATGACGGTACCGTAAGAAATTAAGCACCGGCTAAC  | 497            |          |             |
| QY           | 481          | TACGTGCCAGACGCCGGGTAAATCGTAGGTGTGAACGTTAATCGGAATTACTGGGGGT      | 540            |          |             |

|    |      |   |     |
|----|------|---|-----|
| Db | 498  | TACGGCCAGACGACCGCGGTAAATAGCTAAGGTCGAAAGCCTTAAATCGGAATTTACTGGGCGCT | 555 |
| Oy | 541  | AAAGGCTGCGCAGGGGCGCTTTGTAACTCAGATGTGAATCCCGGGCTTAACTCGGGAAT       | 600 |
| Db | 558  | AAAGGCTGCGCAGGGGCGGTGATGTAAAGCAGTTGTGAATCCCGGGCTCAACTCGGGAAC      | 617 |
| Oy | 601  | TGCGTTTGAACCTAACAGGCTTAGAGTGTGGCAGAGGGAAGTGAATTCATGTGTGCAG        | 660 |
| Db | 618  | TGCATCTGTGACTGCATCGCTGGAATGACGACAGAGGGGAATGGAATTCGCGTGTACAG       | 677 |
| Oy | 661  | TGAATGCGGTAGAGATATGGAAGAAACATCGATGCGCGAAGCAGCCTCTGGGTAACT         | 720 |
| Db | 678  | TGAATGCGGTAGATATGCGGAAGAAACACGATGCGCAAGGCAATCCCGTGGGCTGTACT       | 737 |
| Oy | 721  | GACGCTCATGCAAGAAAGCGTGGGAGCAACAGATTTGATACCTTGGTAGTCCAGCC          | 780 |
| Db | 738  | GACGCTCATGCAAGAAAGCGTGGGAGCAACAGATTTGATACCTTGGTAGTCCAGCC          | 797 |
| Oy | 781  | CTAAACGATGCAACTAGTTGTGTGGCCCTTATTAAGCGTTGGTAAAGCACTAACCGGTGA      | 840 |
| Db | 798  | CTAAACGATGCAACTAGTTGTGTGGCCCTTATTAAGCGTTGGTAAAGCACTAACCGGTGA      | 857 |
| Oy | 841  | AGTTGACCGGCTGGGAGAGTACGGTGCAGAACTTAAACCTCAAGAAATTTAGACGGGACCC     | 900 |
| Db | 858  | AGTTGACCGGCTGGGAGAGTACGGGCGCAAGGTTGAACCTCAAGAAATTTAGACGGGACCC     | 917 |
| Oy | 901  | GCACAAGCGGTGTGATTAATGTGGAATTAATTCGATGCAACGCGAAAACTTACTACCTT       | 960 |
| Db | 918  | GCACAAAGCGGTGTGATTAATGTGGAATTAATTCGATGCAACGCGAAAACTTACTACCTT      | 977 |
| Oy | 961  | GACATGTAGCGCAATTTTCTAGAGATAGATTAGTGCT---TGCGGAACGCTAACAGAGTG      | 101 |
| Db | 978  | GACATGTAGCGCAATTTTCTAGAGATAGATTAGTGCT---TGCGGAACGCTAACAGAGTG      | 103 |
| Oy | 1018 | CTGCATGCGCTGTCGTCAGCTCGTGTCTGTGAGATGTGTGGTTAAATGCCCGCAACGACGA     | 107 |
| Db | 1038 | CTGCATGCGCTGTCGTCAGCTCGTGTCTGTGAGATGTGTGGTTAAATGCCCGCAACGACGA     | 109 |
| Oy | 1078 | ACCTTGTTCATTAATTTGCCATCAATTTGGTTGGGCACTTTAAATGACATCCCGGTACAAA     | 113 |
| Db | 1098 | ACCTTGTTCATTAATTTGGTCTTA-CATTCAGTTGGGCACTTAAATGACATCCCGGTACAAA    | 115 |
| Oy | 1138 | CCGAGGAAGGTGGGAGTAGACGTCAAGTCTCATAGGCCCTTAAAGGTAAGGCTTCACAG       | 119 |
| Db | 1157 | CCGAGGAAGGTGGGAGTAGACGTCAAGTCTCATAGGCCCTTAAAGGTAAGGCTTCACAG       | 121 |
| Oy | 1198 | TAAATCAATGGCGCCTAACAGAGGTTGGCCAACCCGACGAGGGGAGCTAACTCAGAAAC       | 125 |
| Db | 1217 | TCAATCAATGGCTGGTAAACAAAGGTTGGCCAACCCGACGAGGGGAGCTAACTCAGAAAC      | 127 |
| Oy | 1258 | GCGTGTATGTCCGATCCGAGTCTGCACATCTCGATCTCGTGAAGTGGGAATCGCTAGTAAT     | 131 |
| Db | 1277 | CAGTGTATGTCCGATCCGAGTCTGCACATCTCGATCTCGTGAAGTGGGAATCGCTAGTAAT     | 133 |
| Oy | 1318 | CGCGGATAGCAATGCGCGGTAAATACGTTCCCGGGTCTTGAACACACCGCCGCTACAC        | 137 |
| Db | 1337 | CGCGGATAGCAATGCTACGCTAAATACGTTCCCGGGTCTTGAACACACCGCCGCTACAC       | 139 |
| Oy | 1378 | CATGGAGATGGGTTTCAACAGAAAGCAGTATCTAACCTGAAGAGAGGCGCTTGCACGG        | 143 |
| Db | 1397 | CATGGAGATGGGTTTCTGCAGAAAGTATGTTAGCTTAAACGCAAGAGGGGAGTATACACGG     | 145 |
| Oy | 1438 | TGAATTTATGACTGGGGTG 1457  |     |
| Db | 1457 | CAGGATTCGTACTGGGGTG 1476  |     |

RESULT 3  
US-10-515-311-5  
; Sequence 5, Application US/105153111  
; Publication No. US20060030021A1  
; GENERAL INFORMATION:  
; APPLICANT: Turner, Susan J

|    | Query Match   | 74.8%; Score 1089.6; DB 9; Length 1405; |  |
|----|---|---|--|
|    | Best Local Similarity   | 87.2%; Pred. No. 0;                     |  |
|    | Matches 1233; Conservative  | 0; Mismatches 169; Indels 12; Gaps      |  |
| QY | 18 TGCCTTACACATGCAAGTCGAAACGCGACGACGATGCTTGATCTGTGGCGAGTGGCGG     | 77                                      | TITLE OF INVENTION: Novel Microorganisms and Uses Therefor |
| DB | 1 TGCCTTACACATGCAAGTCGAAACGCGTAAC-----AGCTTTCGAGATGCGAAGTGGCGA    | 56                                      | FILE REFERENCE: 11752-006US1                               |
| QY | 78 ACGGATGATGATATCCATCCGGAACGATTCACAAAGAGGGGGGTAAACGATTCGAAAGATG  | 137                                     | CURRENT APPLICATION NUMBER: US/10/515.311                  |
| DB | 57 ACGGATGATGATATCATCGGAACGTGCCCATCGTGGGGGATTAACGAAGCGAAAGCTTTG   | 116                                     | PRIOR FILING DATE: 2004-11-22                              |
| QY | 138 CTAATACCGCATTAATCTCTAAGAGAGAAAGCAGGGGATTCGAAGAAGCTTGCGCTTTTGA | 197                                     | PRIOR APPLICATION NUMBER: PCT/NZ2003/000100                |
| DB | 117 CTAATACCGCATTAATCATGATTCAGGATGGAAGAGGGGACCGGAAGGCTTGGCGCAACGA | 176                                     | PRIOR FILING DATE: 2003-05-22                              |
| QY | 198 GCGGCGCATGCTCTGATTAAGCTAGTTGGTGGGTAAAGGCTTACCAAGCGACGATCACTA  | 257                                     | PRIOR APPLICATION NUMBER: NZ 519137                        |
| DB | 177 GCGGCGCATGCGAATTAAGTATGTTGGTGGGATAAAGCTTACCAAGCGACGATCTGTA    | 236                                     | PRIOR FILING DATE: 2002-05-22                              |
| QY | 258 GTTGCTCTGAGAGAGACCAACCAACCTGGACCTGAGACACGCGCCCAAGCTCCGACGGG   | 317                                     | NUMBER OF SEQ ID NOS: 6                                    |
| DB | 237 GCTGCTCTGAGAGAGACCAACCAACCTGGACCTGAGACACGCGCCCAAGCTCCGACGGG   | 296                                     | SOFTWARE: PatentIn version 3.1                             |
| QY | 318 AGGCACGACGATGGGAAATTTTGAACAATGGGCGCAAGCCTGATCCAGCAATGCCGCTGAG | 377                                     | SEQ ID NO 5  |
| DB | 297 AGGCACGACGATGGGAAATTTTGAACAATGGGCGCAAGCCTGATCCAGCAATGCCGCTGCA | 356                                     | LENGTH: 1405   |
| QY | 378 TGAAGAAAGCCTTCGGGTGTAAAGCTCTTCACTGAGAAAGAAAGTTACGGTAAATA      | 437                                     | TYPE: DNA  |
| DB | 357 GGAAGAAAGCCTTCGGGTGTAAAGCTCTTCACTGAGAAAGAAAGTTACGGTAAATA      | 416                                     | ORGANISM: Acidovorax temperans                             |
| QY | 438 ATCGTACTATGACCGGTATGACAGAAAGAACCGGCTAATCTACGTGCGACGACGCCG     | 497                                     | US-10-515-311-5  |
| DB | 417 CCGGGGCTCATGACCGGTATGACAGAAAGAACCGGCTAATCTACGTGCGACGACGCCG    | 476                                     |  |
| QY | 498 GGTAAATACGTAGGGGTGCAAGCGTAAATCCGAATTAAGGGGCTTAAAGGGGTGCGACGGG | 557                                     |  |
| DB | 477 GGTAAATACGTAGGGGTGCAAGCGTAAATCCGAATTAAGGGGCTTAAAGGGGTGCGACGGG | 536                                     |  |
| QY | 558 CTTTGTAAGTCAGATGTGAATCCCGGGCTTAACTGGGAATTCGTTGAAACTACAA       | 617                                     |  |
| DB | 537 TTTAATAAGACAGATGTGAATCCCGGGCTTAACTGGGAATTCGTTGAAACTGAT        | 596                                     |  |
| QY | 618 GGTAGAGTGTGCGAGAGGAGGTGAATTCATGTGTGAGTGAAGTGAATTCGTAAGATG     | 677                                     |  |
| DB | 597 AGCTAGAGTGTGCGAGAGGAGGATGAATTCGCGGTGTAGACAGTGAATGCGTGAATG     | 656                                     |  |
| QY | 678 TGAAGAAACATCCATGGCGGAAGGACGCTCCGGGTTAAACATGACGCTACATGACGAA    | 737                                     |  |
| DB | 657 CCGAGAAACATCCATGGCGGAAGGACATCCCTGGGCTTGTACATGACGCTACATGACGAA  | 716                                     |  |
| QY | 738 GCGTGGGAGCAAAACAGATTTAGATACCTGTGATGTCACGCGCTTAAACGATGCACTA    | 797                                     |  |
| DB | 717 GCGTGGGAGCAAAACAGATTTAGATACCTGTGATGTCACGCGCTTAAACGATGCACTG    | 776                                     |  |
| QY | 798 GTTGTTGGGCTTATTAAGCTGTGATTAACGAAGCTAACCGCTGAAGTTGACCGCTGGGGA  | 857                                     |  |



QY 1019 TGCATGGCTGTCTGCTGCTGTCTGTGAGATGTTGGTTAAGTCCCGCAACGACCGAA 1078  
 DB 1039 TGCATGGCTGTCTGCTGCTGTCTGTGAGATGTTGGTTAAGTCCCGCAACGACCGAA 1098  
 QY 1079 CCTTTCATTAATTTGCGCATCA--TTTGGTTGGGCACTTTAATGAGACTGCGCGTGACAA 1136  
 DB 1099 CCTTTCATTAATTTGCGCATCA--TTTGGTTGGGCACTTTAATGAGACTGCGCGTGACAA 1158  
 QY 1137 ACCGAGAGAGAGTGGGAGATGACGTCAAGTCTCATGCGCTTTAATGAGAGGCTTTCACAC 1196  
 DB 1159 ACCGAGAGAGAGTGGGAGATGACGTCAAGTCTCATGCGCTTTAATGAGAGGCTTTCACAC 1218  
 QY 1197 GATATACAAATGGGCGGTATGACAGAGGTTGGCAACCGCGAGGGGAGCTAATCTGAGAAAG 1256  
 DB 1219 GTGTCTACAAATGGTGTGATGACAGAGGTTGGCAACCGCGAGGGTGAATCTGACAA 1278  
 QY 1257 CGCGTCTGAGTCCCGATCGAGTCTGCAACTGCACTCCGTGAGTGGAGATCGCTAGTAA 1316  
 DB 1279 CGCATCTGATGCCGATCGCAGTCTGCAACTGCACTGCTGATGAGTCCGGAATCGCTAGTAA 1338  
 QY 1317 TCGCGATTCAGCATGTGCGGAGTAAATGCTTCCGCGCTTTGTAACAACCGCCGCTGACA 1376  
 DB 1339 TCGCGATTCAGCATGTGCGGAGTAAATGCTTCCGCGCTTTGTAACAACCGCCGCTGACA 1398  
 QY 1377 CCATGGAGAGGCTTTTCAACCAAGAGAGTGTCTAACCCTAAGAGAGGCGCTTGCCACG 1436  
 DB 1399 CCATGGAGAGGCTTTTCAACCAAGAGAGTGTCTAACCCTAAGAGAGGCGCTTGCCACG 1458  
 QY 1437 GTGAGATTTCATGACTGGGGTG 1457  
 DB 1459 GTGAGATTTCATGACTGGGGTG 1479

## RESULT 5

US-10-831-286A-48683  
 ; Sequence 48683, Application US/10831286A  
 ; Publication No. US20060046246A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ZENG, QIANDONG  
 ; APPLICANT: CHATELIER, SONIA  
 ; APPLICANT: MOIR, DONALD T.  
 ; APPLICANT: LACROIX, BRUNA  
 ; APPLICANT: CHIDRESS, DARRIEL  
 ; TITLE OF INVENTION: GENUS, GROUP, SPECIES AND/OR STRAIN SPECIFIC 16S rDNA SEQUENCES  
 ; FILE REFERENCE: 032796-174.001  
 ; CURRENT APPLICATION NUMBER: US/10/831.286A  
 ; PRIOR FILING DATE: 2004-04-26  
 ; PRIOR APPLICATION NUMBER: 60/464,955  
 ; NUMBER OF SEQ ID NOS: 48788  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 48683  
 ; LENGTH: 1493  
 ; TYPE: DNA  
 ; ORGANISM: *Paenococcus dispersa*  
 US-10-831-286A-48683

Query Match 70.1%; Score 1021.2; DB 9; Length 1493;  
 Best Local Similarity 82.9%; Pred. No. 2.5e-309;  
 Matches 1214; Conservative 0; Mismatches 243; Indels 7; Gaps 4;

QY 1 ATTGAACGCTGGCGGCAATGCTTTACATGCAATGCAAGTCCGACGACGAGTCTTG--- 57  
 DB 1 ATTGAACGCTGGCGGCGGCAATGCTTTACATGCAATGCAAGTCCGACGACGAGTCTTGCG 60  
 QY 58 -CATCTGCTGGCGAGTGGCGGAGCGGAGTGAATGATCGGAAAGTATCCGAAAGAGAGG 116  
 DB 61 TCTTTGGGTGGCGAGTGGCGGAGCGGAGTGAATGATCTGCGAAACTGCGCATGAGAGG 120  
 QY 117 GGTAAACCATCGAAAGATGTGCTAATAACCGCATATCTTAAAGAGAGAAAGCAGGGATC 176  
 DB 121 GATTAATCTAGGAAACGCTAGCTAATAACCGCATATCTTAAAGAGAGAAAGTGGGGAGCC 180

QY 177 GAAAGACCTTGGCGCTTTTGGAGCGCGCATGCTGATTAAGTGTGGGGGTAAGAGGC 236  
 DB 181 TTGGGCTTCAACCATCGGATGTGTCAGATGGAGTACTGATGATGGGTAATGCGC 240  
 QY 237 CTACCAAGCGAGATCAGTATGTTGGTCTGAGAGAGAGCAGACAGCACTCTGGACTGAGA 296  
 DB 241 TCACTTAGGAGAGATCTTACGCTGGTCTGAGAGATGACAGACAGCACTCTGGAATCTAGA 300  
 QY 297 CAGGCGCCAGACTCTTACGAGAGAGCAGTGGGGAAATTTGACAAATGGGCGCAAGCCT 356  
 DB 301 CAGGCTCCAGACTCTTACGAGAGAGCAGTGGGGAAATTTGACAAATGGGCGCAAGCCT 360  
 QY 357 GATCCAGCAATGCGCGGTGAGTGAAGAGGCTTCCGGTTGTAAGCTTTTCAAGTCCGAG 416  
 DB 361 GATCCAGCAATGCGCGGTGAGTGAAGAGGCTTCCGGTTGTAAGCTTTTCAAGTCCGAG 420  
 QY 417 AAGAAAGGTTACGATTAATATGTAATCTGACTCATGACGATTCGACAGAGAGCAACCGGC 476  
 DB 421 AAGAAAGGTTACGATTAATATGTAATCTGACTCATGACGATTCGACAGAGAGCAACCGGC 480  
 QY 477 TAACTAGTCCAGCAGCGCGGTAAATGCTAGGGTTCAGAGCTTAATCGGAATTAATG 536  
 DB 481 TAACTAGTCCAGCAGCGCGGTAAATGCTAGGGTTCAGAGCTTAATCGGAATTAATG 540  
 QY 537 GCGTAAAGGTTGGCGAGCGCGCTTTGTAAGTCAAGTGTGAATCCCGGGCTTAACCTGG 596  
 DB 541 GCGTAAAGGTTGGCGAGCGCGCTTTGTAAGTCAAGTGTGAATCCCGGGCTTAACCTGG 600  
 QY 597 GAATTCGTTTGAATCAACAGGCTAGAGTGTGGCAGAGAGAGGAGTGAATTCATGTGTA 656  
 DB 601 GAATTCGTTTGAATCAACAGGCTAGAGTGTGGCAGAGAGAGGAGTGAATTCATGTGTA 660  
 QY 657 GCAGTGAATGCTGATGATATGAAAGACATGATGCGAGAGCGACCTCTCTGGGTTAA 716  
 DB 661 GCAGTGAATGCTGATGATATGAAAGACATGATGCGAGAGCGACCTCTCTGGGTTAA 720  
 QY 717 CACTGACGCTCATGACAGAAAGGCTGGGGAGCAACAGATTGATTAACCTGGTGAATGCA 776  
 DB 721 GACTGACGCTCATGAGAGAGGCTGGGGAGCAACAGATTGATTAACCTGGTGAATGCA 780  
 QY 777 CGCCTTAAACGATGCTCACTAGTATGTTGGCGCTTAATTAAGCTTGG-TAAAGAGCTAACG 835  
 DB 781 CGCCTTAAACGATGCTCACTAGTATGTTGGCGCTTGAAGCTTGGCGAGCTAACG 840  
 QY 836 CTTGAAGTTGACCGCTGGGAGTACGCTGCGCAAGTTAACTCAAAGAAATTGACGGG 895  
 DB 841 CTTGAAGTTGACCGCTGGGAGTACGCTGCGCAAGTTAACTCAAAGAAATTGACGGG 900  
 QY 896 GACCCGACAGCGGTGAGATTATGAGATTAAATGATGCAAGCGAAAAAAGCTTAACCTTA 955  
 DB 901 GACCCGACAGCGGTGAGATTATGAGATTAAATGATGCAAGCGAAAAAAGCTTAACCTTA 960  
 QY 956 CCTTGAACATGATGCAATTTTCTAGAGATTAATTAAGTGTG-TCTTGGGAAAGCTTAACAG 1014  
 DB 961 CCTTGAACATGATGCAATTTTCTAGAGATTAATTAAGTGTG-TCTTGGGAAAGCTTAACAG 1020  
 QY 1015 GTCTGATGAGTGTGCTGATGCTGCTGCTGAGATGTTGGTTAAGTCCGCAACGAGC 1074  
 DB 1021 GTCTGATGAGTGTGCTGATGCTGCTGCTGAGATGTTGGTTAAGTCCGCAACGAGC 1080  
 QY 1075 GCAACCTTGTCACTTAATTAATGCAATC-ATTGTTGGGCACTTAATGAGACTGCGGTGA 1133  
 DB 1081 GCAACCTTGTCACTTATTTGTCAGAGCGGTTCGCGGAACTCAAAGAGACTGCGGTGA 1140  
 QY 1134 CAACCGGAGAGAGTGGGAGATGACGTCAAGTCTTCATGAGCTTATGAGTGGTGAAGGCTTCA 1193  
 DB 1141 TAAACGGAGAGAGTGGGAGATGACGTCAAGTCTTCATGAGCTTATGAGTGGTGAAGGCTTCA 1200  
 QY 1194 CACGTATATCAATGAGCGGTACAGAGGTTTCCAAACCGCGAGGAGGAGTAAATCTCAGA 1253  
 DB 1201 CACGTCTCAATATGCGCATATCAAAAGAGAGGAGCTTCGAGAGAGCAAGCGGACCTCATA 1260

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QY 1254 AACCGGTCTAGTCCGGATCGGAGTCTGCACTCCGTAAGTCCGATCGTAG 1313
DB 1261 AACTGGGTCTAGTCCGGATCGGAGTCTGCACTCCGTAAGTCCGATCGTAG 1320
QY 1314 TAATCGGATGAGATGTCGCGGTGAATACGTTCCGGGTCTTGTACACGCCCGTC 1373
DB 1321 TAATCGTATGATCAAGATGCTACCGGTGAATACGTTCCGGGTCTTGTACACGCCCGTC 1380
QY 1374 ACAACATGAGAGTGGGTTTCAACCAAGAGTATGCTAAACGTAAGAGGGCGCTTGCC 1433
DB 1381 ACAACATGAGAGTGGGTTTCAACCAAGAGTATGCTAAACGTAAGAGGGCGCTTGACC 1440
QY 1434 ACGGTAGATTCACTGACTGGGGTG 1457
DB 1441 ACTTGTGATTCACTGACTGGGGTG 1464

RESULT 6
US-10-831-286A-48685
/ Sequence 48685, Application US/10831286A
/ Publication No. US20060046246A1
/ GENERAL INFORMATION:
/ APPLICANT: ZENG, QIANDONG
/ APPLICANT: CHATELLIER, SONIA
/ APPLICANT: MOIR, DONALD T.
/ APPLICANT: LACROIX, BRUNA
/ APPLICANT: CHILDRESS, DARRELL
/ TITLE OF INVENTION: GENUS, GROUP, SPECIES AND/OR STRAIN SPECIFIC 16S rDNA SEQUENCES
/ FILE REFERENCE: 032796-174.001
/ CURRENT APPLICATION NUMBER: US/10/831,286A
/ CURRENT FILING DATE: 2004-04-26
/ PRIOR APPLICATION NUMBER: 60/464,955
/ PRIOR FILING DATE: 2003-04-24
/ NUMBER OF SEQ ID NOS: 48788
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 48685
/ LENGTH: 1508
/ TYPE: DNA
/ ORGANISM: Providencia rustigianii
/ US-10-831-286A-48685

Query Match 70.0%; Score 1020.2; DB 9; Length 1508;
Best Local Similarity 83.3%; Pred. No. 5.2e-309;
Matches 1219; Conservative 0; Mismatches 238; Indels 6; Gaps 5;

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QY 419 GAAAGGTTAGGTAATATATGATGACTGACGAGTATCGACAGAGAAAGACCGGCTA 478
DB 431 GAAGGCTTGAATGCTATATATGCTCAACATTAACCTTACCAACAGAAAGACCGGCTA 490
QY 479 ACTACGTGACAGACCGCGGGTAATACGTAAGGTGCAACGTTAATCGAATTTACTGGGC 538
DB 491 ACTCGGTGACAGACCGCGGGTAATACGTAAGGTGCAACGTTAATCGAATTTACTGGGC 550
QY 539 GTAAAGGTCGCGAGCGGCTTGTAACTCAATGTGAATATCCCGGGCTTAACTCGGGA 598
DB 551 GTAAAGGTCGCGAGCGGCTTGTAACTCAATGTGAATATCCCGGGCTTAACTCGGGA 610
QY 599 ATTGGCTTGAACCTAACAAGGCTAGAGTGTGACAGAGGAGGTGAAATTCATGTTAGC 658
DB 611 ATGGCACTTAAGCTGTGTAGCTAGCTAGATCTTGTAGAGGGGGGTAAATTCATGTTAGC 670
QY 659 AGTGAATGCTAGATATGGAAGAACATCATAGGCGAAGGCAAGCTTCCTGGGTTTACA 718
DB 671 GGTGAATGCTAGATATGGAAGAACATCATAGGCGAAGGCGGCGCCCTGGACAAAGA 730
QY 719 CTGACGCTATGACAGAAAGCGTGGGAGCAACAGATTAATACCTGTGATGTCACG 778
DB 731 CTGACGCTATGACAGAAAGCGTGGGAGCAACAGATTAATACCTGTGATGTCACG 790
QY 779 CCTTAAGATGTCACATGATGTTGGGCTTATAGGCTTGA-TAACAGATAACGCG 837
DB 791 CTGTAAACATGTCATGATGTTGGAGTGTTCCTTGAAGAGTGGCTTCCGAGTAAACGCG 850
QY 838 TGAAGTTGACCGCTGGGAGTACGCTCGCAAGATTAAACTCAAGAAATTGACGGGA 897
DB 851 TTAATGACCGCGCTGGGAGTACGCGCGCAAGGTTAAATCAATGAATTGACGGGG 910
QY 898 CCGGCAAGCGGTGATTAATGATTAATTCATGACGCAAGCAAACTTAATCTTACC 957
DB 911 CCGGCAAGCGGTGATGATGTTAATTCATGACGCAAGCAAACTTAATCTTACC 970
QY 958 CTGACATGATGAAATTTTCTAGAGATGATTAAGT-CTTGGGAGAACCTTAACACAGGT 1016
DB 971 CTGACATGATGAAATTTTCTAGAGATGATTAAGTCTTGGGAGAACCTTAACACAGGT 1030
QY 1017 GGTGATGCTGTCGTCAGCTGTCGTGAGATGTTGGGTTAAGTCCGCAACGAGCGC 1076
DB 1031 GGTGATGCTGTCGTCAGCTGTCGTGAGATGTTGGGTTAAGTCCGCAACGAGCGC 1090
QY 1077 AACCTTGCATTAATGTCATCA--TTTGTGTTGGGCACTTAATTAAGATCTGGGTAC 1134
DB 1091 AACCTTGCATTAATGTCATCA--TTTGTGTTGGGCACTTAATTAAGATCTGGGTAC 1150
QY 1135 AAACCGAGAGAGTGGGATGACGTCAGTCAAGTCCGCTTAATGGGTAGGGCTTAC 1194
DB 1151 AAACCGAGAGAGTGGGATGACGTCAGTCAAGTCCGCTTAATGGGTAGGGCTTAC 1210
QY 1195 ACGTAAATACATGCGCGTACAGAGGTTGCCAACCGCGAGAGGGAGCTAATCTCAGA 1254
DB 1211 ACGTAAATACATGCGCGTACAGAGGTTGCCAACCGCGAGAGGGAGCTAATCTCAGA 1270
QY 1255 AGCGGTGCTAGTCCGATCGAGTCTGCACTCGACTCCGTGAAGTCCGTAAGT 1314
DB 1271 AGCGGTGCTAGTCCGATCGAGTCTGCACTCGACTCCGTGAAGTCCGTAAGT 1330
QY 1315 AATCGGATGACAGATGTCGCGGTGAATGTTCCCGGGCTTGTACACACCGCCGTC 1374
DB 1331 AATCGGATGACAGATGTCGCGGTGAATGTTCCCGGGCTTGTACACACCGCCGTC 1390
QY 1375 CACCATGAGAGTGGTTTCAACAGAAAGCTAATCGTAAGAGGGCGCTTGCA 1434
DB 1391 CACCATGAGAGTGGTTTCAACAGAAAGCTAATCGTAAGAGGGCGCTTGCA 1450
QY 1435 CCGTGAATTCATGACTGGGGTG 1457
DB 1451 CTTTGTGATTCACTGACTGGGGTG 1473

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SOFTWARE: PatentIn version 3.2

SEQ ID NO 48681

LENGTH: 1494

TYPE: DNA

ORGANISM: Pantoea dispersa

US-10-831-286A-48681

Query Match 70.0%; Score 1019.6; DB 9; Length 1494;

Best Local Similarity 82.9%; Pred. No. 8e-309;

Matches 1213; Conservative 0; Mismatches 244; Indels 7; Gaps 4;

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QY 1 ATGAAAGCGTGGGGGCGATGCTTTACATGCAAGTGCAGCGGACGAGTCTT--- 57
DB 1 ATGAAAGCGTGGGGGCGGCTTAACATGCAAGTGCAGCGGACGAGAGAGCTTGC 60
QY 58 -CATCTGGTGGCGAGTGGCGGACGGGTGATGATGATCGGAAAGTATCGAAGAGGG 116
DB 61 TCTTTGGGTGGCGAGTGGCGGACGGGTGATGATGATGATGATGATGATGATGAT 120
QY 117 GGTAAAGCATGCAAGATGCTTAATACCGCATTAATCTTAAGAGAGAAAGAGGATC 176
DB 121 GATTAATCACTGGAAGACGCTAATACCGCATTAATCTTAAGAGAGAAAGAGGATC 180
QY 177 GAAAGACCTTGGCTTTTGAAGGCGCGATGCTGATTAAGTGTGGGGGTAAGGC 236
DB 181 TTGGGGCTTCAACCATGATGATGCTTCAAGTGGGATTAAGTGTGGGGGTAAGGC 240
QY 237 CTACCAAGCGGACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 296
DB 241 TCACTTAAGGCGAGTATCTTAAGTGTGATGATGATGATGATGATGATGATGATGAT 300
QY 297 CACGGCCAGATCTTAAGGAGGCGAGATGAGGAGAAATTTGCAATGGGCGCAAGCT 356
DB 301 CACGGCTCAACATCTTAAGGAGGCGAGATGAGGAGAAATTTGCAATGGGCGCAAGCT 360
QY 357 GATCCAGCATGCGCGGTGATGAGGAGGAGGCTTGGGTTGTAAGCTTTTCACTGAG 416
DB 361 GATCCAGCATGCGCGGTGATGAGGAGGAGGCTTGGGTTGTAAGCTTTTCACTGAG 420
QY 417 AAGAAAGGTTACGGTAATTAATGCTGATCATAGACGCTATCGACAGAGAGACCGGC 476
DB 421 AGAAGGCGGTGAGGTTAATTAATGCTGATCATAGACGCTATCGACAGAGAGACCGGC 480
QY 477 TAACTACGTGCGCAGACGCGCGGTAATTAATGATGATGATGATGATGATGATGAT 536
DB 481 TAACTACGTGCGCAGACGCGCGGTAATTAATGATGATGATGATGATGATGATGAT 540
QY 537 GCGTAAAGGTTGGCGAGGCGGCTTTGTAAGTCAAGATGTAATCCCGGGCTTAACCTGG 596
DB 541 GCGTAAAGGTTGGCGAGGCGGCTTTGTAAGTCAAGATGTAATCCCGGGCTTAACCTGG 600
QY 597 GAAATGCGTTGAAACTTAAGGCTAGATGATGATGATGATGATGATGATGATGATGAT 656
DB 601 GAAATGCGTTGAAACTTAAGGCTAGATGATGATGATGATGATGATGATGATGATGAT 660
QY 657 GCACTGAATGCGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 716
DB 661 GCGGTGAATGCGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
QY 717 CACTGAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 776
DB 721 GACTGAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
QY 777 GCGCCTTAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 835
DB 781 GCGCCTTAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
QY 836 CCGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 895
DB 841 CCGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
QY 896 GACCCGACAGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 955

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DB 901 GCGCCGACAGCGGTGAGCATGCTTTAATTCGATGCAACGCGAAGACCTTACTG 960
QY 956 CCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1014
DB 961 GCGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
QY 1015 GTCGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1074
DB 1021 GTCGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
QY 1075 GCAACCTTGTATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1133
DB 1081 GCAACCTTGTATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
QY 1134 CAACCGGAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1193
DB 1141 TAAACCGGAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
QY 1194 CAGTGAATCAATGAGGCGGATGATGATGATGATGATGATGATGATGATGATGATGAT 1253
DB 1201 CAGTGAATCAATGAGGCGGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
QY 1254 AAGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1313
DB 1261 AAGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
QY 1314 TAAATGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1373
DB 1321 TAAATGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1380
QY 1374 ACAACGATGAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1433
DB 1381 ACAACGATGAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
QY 1434 ACGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1497
DB 1441 ACTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1464

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RESULT 9

US-10-831-286A-48677

Sequence 48677, Application US/10831286A

Publication No. US2006046246A1

GENERAL INFORMATION:

APPLICANT: ZENG, QIANDONG

APPLICANT: CHATELLIER, SONIA

APPLICANT: MOIR, DONALD T.

APPLICANT: LACROIX, BRUNA

APPLICANT: CHILDRESS, DARELL

TITLE OF INVENTION: GENUS, GROUP, SPECIES AND/OR STRAIN SPECIFIC 16S rDNA SEQUENCES

FILE REFERENCE: 032796-174.001

CURRENT APPLICATION NUMBER: US/10/831, 286A

PRIOR FILING DATE: 2004-04-26

PRIOR APPLICATION NUMBER: 60/464,955

NUMBER OF SEQ ID NOS: 48788

SOFTWARE: PatentIn version 3.2

SEQ ID NO 48677

LENGTH: 1507

TYPE: DNA

ORGANISM: Providencia rettgeri

US-10-831-286A-48677

Query Match 69.9%; Score 1018; DB 9; Length 1507;

Best Local Similarity 83.2%; Pred. No. 2.6e-308;

Matches 1217; Conservative 0; Mismatches 240; Indels 5; Gaps 5;

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QY 1 ATGAAAGCGTGGGGGCGATGCTTTACATGCAAGTGCAGCGGACGAGTCTTGA 59
DB 11 ATGAAAGCGTGGGGGCGGCTTAACATGCAAGTGCAGCGGACGAGTCTTGTCT 70
QY 60 TCTGG-TGGCGAGTGGCGGACGGGTGATGATGATGATGATGATGATGATGATGATGAT 118

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Db      71 TCTGCTGACGAGCGCGGACGCGGTGAGTAATGTATGAGGAGATCTGCCGATAGAGGGGGA 130
Qy      119 TAAAGCATCGAAAGATGTGCTAATACCGCATATATCTTAAGAGAAAGCAGGGGATGGA 178
Db      131 TAAACACAGGAAACGGTGTAAATACCGCATATATCTTAAGAGAAAGCAGGGGAACTT 190
Qy      179 AAGACCTTGCGCTTTTGGAGCGGCGATGTCTGATTAGTAGTGTGGGGGTAAGGCGCT 238
Db      191 CGGTCTTGCGCTATCGAATGAACCCATATAGGGAATTAGTAGTAGTGAAGTAAATGCGCTC 250
Qy      239 ACCAAGGCGACGATCAGTAGTGTGTCTGAGAGGACGACGACACTGGGACTGAGACA 298
Db      251 ACTTAGGCGACGATCCTAGCTGTGTCTGAGAGGATGATCAGGCACTGGGACTGAGACA 310
Qy      299 CGGCGCCAGACTCTTAACGGGAGGACGACATGGGGGAAATTTTGGACATGGGCGGCAAGCTTGA 358
Db      311 CGGCGCCAGACTCTTAACGGGAGGACGACATGGGGGAAATTTTGGACATGGGCGGCAAGCTTGA 370
Qy      359 TCCAGCAATGCGCGGTGAGTGAAGAAAGGCTTCGGGCTTGAAGGCTCTTTCAGTCAAGAA 418
Db      371 TGCAGCCATGCGCGGTGAGTGAAGAAAGGCTTCGGGCTTGAAGGCTCTTTCAGTCAAGAA 430
Qy      419 GAAAGGTTACGTAATATATGATCTCATGACGGTATCGACAGAGAAAGCACCGGCTTA 478
Db      431 GAAAGGTTACGTAATATATGATCTCATGACGGTATCGACAGAGAAAGCACCGGCTTA 490
Qy      479 ACTAGCTGCCAGACGCGCGGTAAATAGTAGGTTCAGAGCTTAAATCGGAATTAATCTGGGC 538
Db      491 ACTCGGTGCCAGACGCGCGGTAAATAGTAGGTTCAGAGCTTAAATCGGAATTAATCTGGGC 550
Qy      539 GTAAAGGTTGCGCAGGCGGCTTTGTAGTCAAGATGTGAATTCGCCGGGCTTAACCTGGGA 598
Db      551 GTAAAGGTTGCGCAGGCGGCTTTGTAGTCAAGATGTGAATTCGCCGGGCTTAACCTGGGA 610
Qy      599 ATTGCGTTTGAACATAAGGCTAGAGTGTGACAGAGGAGAGTGAATTCATGTGTAGC 658
Db      611 ATGCGATCTAAGACTGTGTGACAGTCTTGTAGAGGGGGTGAATTCATGTGTAGC 670
Qy      659 AGTGAATGCTTAAGATATGGAAGAAATGATGTGCGAAGGCGAGCTTCCTGGTTAAACA 718
Db      671 GGTGAATGCTTAAGATATGGAAGAAATGATGTGCGAAGGCGAGCTTCCTGGTTAAACA 730
Qy      719 CTGACGCTCATGCAAGAAAGGTTGGGAGCAAAACAGATTGATPACCTGGTATGCCAG 778
Db      731 CTGACGCTCATGCGAGGCGGAGGAGGAGCAAAACAGATTGATPACCTGGTATGCCAG 790
Qy      779 CCTTAAACGATGTC-AACTAGTGTGTGGGCTTATTAAGCTTGTGTAACGAAGCTTAACGCG 837
Db      791 CTGTAACGATGTGATTTGAGGTTGTTCCCTAGAGAGTGGCTTCGGAAGCTTAACGCG 850
Qy      838 TGAAGTTGACCGGCTGGGAGATAGGTTGCAAGATTAAACTCAAGGAATTGACGGGGA 897
Db      851 TTAATATGACCGGCTGGGAGATAGGTTGCAAGATTAAACTCAATGAATTTGACGGGGA 910
Qy      898 CCGGCAAGAGGTTGATTAATTCGATGCAAGCGGAAAAACCTTACCTACC 957
Db      911 CCGGCAAGAGGTTGATTAATTCGATGCAAGCGGAAAAACCTTACCTACC 970
Qy      958 CTGACATGTAGCGAATTTTCTAGAGATGAATTAATG-CTTCGGGAAGCTTACACAGGT 1016
Db      971 CTGACATGTAGCGAATTTTCTAGAGATGAATTAATG-CTTCGGGAAGCTTACACAGGT 1030
Qy      1017 GGTGCAATGCTGTGTGATCGGTGTGTGAGATGTTGGGTTAAAGTCCCGCAAGAGCGC 1076
Db      1031 GGTGCAATGCTGTGTGATCGGTGTGTGAGATGTTGGGTTAAAGTCCCGCAAGAGCGC 1090
Qy      1077 AACCTTGCTAATATTGCAATC-ATTGTTGGGCACTTAAATAGACCTCGGTGACA 1135
Db      1091 AACCTTGCTAATATTGCTTCCAGCATACGTCGGGAATCAAAAGAGACTCCGCTGATA 1150
Qy      1136 AACCGAGAGAGGTGGGATGACGTCAAGTCTCAAGGCGCTTATGGTGAAGGCTTCA 1195
Db      1151 AACCGAGAGAGGTGGGATGACGTCAAGTCTCAAGTCTCAAGTGAAGGCTTCA 1210

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Qy      1196 CGTAAATCAATGAGCGGTACAGAGGTTGGCAACCCGGAGAGGGAGCTAATCTCAGAA 1255
Db      1211 GGTGCTCAATGAGGCTATACAAAGAGACGACTCGGAGAGCAAGCGGAATCATATAA 1270
Qy      1256 GCGGCTGTAGTCCGATTCGAGTCTGCAACTCGACTCCGTGAAGTCGGAATCGTAGTA 1315
Db      1271 GTAGCTGTAGTCCGATTCGAGTCTGCAACTCGACTCCGTGAAGTCGGAATCGTAGTA 1330
Qy      1316 ATCGCGGATCAGCATGTGCGGCTGAATPAGTTCCCGGCTCTTGAACACACCGCCGTAC 1375
Db      1331 ATCGTGAATCAGAAATGCTACGCTGAATACGTTCCCGGCTCTTGAACACACCGCCGTAC 1390
Qy      1376 ACCATGGAGAGGCTTCAACAGAGAGGTAAGTAAACGTAAGAGAGGCGCTTGGCAC 1435
Db      1391 ACCATGGAGAGGCTTCAACAGAGAGGTAAGTAAACGTTCCCGGAGGCGCTTACAC 1450
Qy      1436 GGTGAGATTGATGACTGGGGTG 1457
Db      1451 TTTGTGATTCATGACTGGGGTG 1472

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RESULT 10
US-10-831-286A-48684
; Sequence 48684, Application US/10831286A
; Publication No. US20060046246A1
; GENERAL INFORMATION:
; APPLICANT: ZENG, QIANDONG
; APPLICANT: CHATELIER, SONIA
; APPLICANT: MOIR, DONALD T.
; APPLICANT: LACROIX, BRUNA
; APPLICANT: CHILDRESS, DARRELL
; TITLE OR INVENTION: GENUS, GROUP, SPECIES AND/OR STRAIN SPECIFIC 16S rDNA SEQUENCES
; FILE REFERENCE: 032796-174.001
; CURRENT APPLICATION NUMBER: US/10/831,286A
; PRIOR APPLICATION NUMBER: 2004-04-26
; PRIOR FILING DATE: 2003-04-24
; NUMBER OF SEQ ID NOS: 48788
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48684
; LENGTH: 1508
; TYPE: DNA
; ORGANISM: Providencia rustigianii
US-10-831-286A-48684

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Query Match      69.8%; Score 1017; DB 9; Length 1508;
Best Local Similarity 83.2%; Pred. No. 5.3e-308;
Matches 1217; Conservative 0; Mismatches 240; Indels 6; Gaps 5;

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Qy      1 ATTGAACGCTGGCGGCAATGCTTTACACATGCAAGTCGACGACAC-AGATGCTTGCA 59
Db      11 ATTGAACGCTGGCGGCGGCAATGCTTTACACATGCAAGTCGACGACAGGGAAGCTTGCT 70
Qy      60 TCGG-AGGAGAGGAGGAGCGGAGTGAATGATGATGCAAGATCAGAAAGAGGGGG 118
Db      71 TCTGCTGACGAGGAGGAGCGGAGCGGAGTGAATGATGATGAGGAGATCTGCCGATAGAGGGGA 130
Qy      119 TAAAGCATCGAAAGATGTGCTAATACCGCATATATCTTAAGAGAAAGCAGGGGATGGA 178
Db      131 TAAAGCATCGAAAGATGTGCTAATACCGCATATATCTTGAAGCAAGAGGGGAATCTT 190
Qy      179 AAGACCTTGCGCTTTTGGAGCGGCGCATGTCTAATTAAGTAAAGTGTGGGTAAAGGCGCT 238
Db      191 CGGTCTTGCGCTATCGGATGAACCAATATGGAATTAGTGTGGGTAAATGAGCTC 250
Qy      239 ACCAAGGCGAGATCAGTAGTGTGTGAGAGGACGACGACCACTGGGAGCTGAGACA 298
Db      251 ACCAAGGCGAGATCCTAGCTGTGTGAGAGGATGATCAGCACTGGGAGCTGAGACA 310
Qy      299 CGGCGCCAGACTCTTACGGAGGAGGACGAGTGGGAATTTTGAACAATGGGCGCAAGCTTGA 358
Db      311 CGGCGCCAGACTCTTACGGAGGAGGACGAGTGGGAATTTTGAACAATGGGCGCAAGCTTGA 370

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QY 359 TCACAGCATCCCGGTGATGAGAGAGCCCTTCCGGTTGTAAGCTCTTTCACTGCGAA 418
DB 371 TGACGCATGCCCGGTGTATGAGAGAGCCCTTCCGGTTGTAAGCTCTTTCACTGCGAG 430
QY 419 GAAAGGTTACGGTAATTAATCGTGACTCAATGACGGTATGACAGAGAGAGCCGGCTA 478
DB 431 GAAAGGTTATGATCTATATCATCAGGATTTGACGTTTACCAAGAGAGAGAGCCGGCTA 490
QY 479 ACTACGTGACAGAGCCCGGTATATACGTAGGTTGCAAGCGTTATTCGAATTACTGGGC 538
DB 491 ACTCCGTGACAGAGCCCGGTATATACGTAGGTTGCAAGCGTTATTCGAATTACTGGGC 550
QY 539 GTTAAAGGTTGCGAGAGCGGCTTTGTAGTCAAGATGTGAATCCCGGGCTTAACTTGGGA 598
DB 551 GTTAAAGGTTGCGAGAGCGGCTTTGTAGTCAAGATGTGAATCCCGGGCTTAACTTGGGA 610
QY 599 ATTGCGTTTAAACTACAGAGGCTAGATGTGCGACAGAGGATGGAATTCATGTGTAGC 658
DB 611 ATGGCATCTAAGACTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 670
QY 659 AGTGAATGCGTGAAGATATGAAAGAACATGATGCGGAAAGCGCTCTCGGTTACA 718
DB 671 GGTGAATGCGTGAAGATATGAAAGAACATGATGCGGAAAGCGCTCTCGGTTACA 730
QY 719 CTGACGCTCATGACGAAAGCGTGGGAGGAAACAGATTAAGATACCTGTGTAGTCCAGC 778
DB 731 CTGACGCTCATGACGAAAGCGTGGGAGGAAACAGATTAAGATACCTGTGTAGTCCAGC 790
QY 779 CCTTAAACGATGATCACTAGTGTGGGCTTATTTAGGCTTGG-TAACGAAGCTAACGCG 837
DB 791 CTGTAAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 850
QY 838 TGAAGTTGACCGCTGCGGAGTAACTGCGTGAAGTTAACTCAAGAGAAATTAACGGGGA 897
DB 851 TTAATGACCGCTGCGGAGTAACTGCGTGAAGTTAACTCAAGAGAAATTAACGGGGA 910
QY 898 CCGGCAACAGCGGTGATTTATGATGATTTATGATGATGATGATGATGATGATGATGATGAT 957
DB 911 CCGGCAACAGCGGTGATTTATGATGATTTATGATGATGATGATGATGATGATGATGATGAT 970
QY 958 CTGACATGATGATGATTTTCTAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1016
DB 971 CTGACATGATGATGATTTTCTAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1030
QY 1017 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1076
DB 1031 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1090
QY 1077 AACCTTGTGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1134
DB 1091 AACCTTGTGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1150
QY 1135 AACCGGAGAGAGGTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1194
DB 1151 AACCGGAGAGAGGTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1210
QY 1195 AGCTTAATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1254
DB 1211 AGCTTAATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1270
QY 1255 AGGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1314
DB 1271 AGGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1330
QY 1315 AATGCGGATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1374
DB 1331 AATGCGGATCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1390
QY 1375 CACCATGAGAGTGGGTTTCAACAGAGAGATGATGATGATGATGATGATGATGATGATGAT 1434
DB 1391 CACCATGAGAGTGGGTTTCAACAGAGAGATGATGATGATGATGATGATGATGATGATGAT 1450

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QY 1435 CGGTGATTCATGATGAGGCTG 1457
DB 1451 CTTTGATTCATGATGAGGCTG 1473

RESULT 11
US-10-831-286A-48682
; Sequence 48682, Application US/10831286A
; Publication No. US20060046246A1
; GENERAL INFORMATION:
; APPLICANT: ZENG, QIANDONG
; APPLICANT: CHATELLIER, SONIA
; APPLICANT: MOIR, DONALD T.
; APPLICANT: LACROIX, BRUNA
; APPLICANT: CHILDRESS, DARELL
; TITLE OF INVENTION: GENUS, GROUP, SPECIES AND/OR STRAIN SPECIFIC 16S rDNA SEQUENCES
; FILE REFERENCE: 032796-174, 001
; CURRENT FILING DATE: 2004-04-26
; PRIOR APPLICATION NUMBER: US/10/831, 286A
; PRIOR FILING DATE: 2003-04-24
; NUMBER OF SEQ ID NOS: 48786
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48682
; LENGTH: 1510
; TYPE: DNA
; ORGANISM: Moellerella wisconsensis
US-10-831-286A-48682

Query Match 69.7%; Score 1015.4; DB 9; Length 1510;
Best Local Similarity 82.7%; Pred. No. 1.7e-307;
Matches 1211; Conservative 0; Mismatches 246; Indels 8; Gaps 4;

QY 1 ATTGAACGCTGCGGCGATCTTTACATGCAATGTAACGCGACAGATGCTTGA- 59
DB 11 ATTGAACGCTGCGGCGATCTTTACATGCAATGTAACGCGACAGATGCTTGC 70
QY 60 ---TCGTGGGAGAGGCGGAGCGGCTGATGATGATGATGATGATGATGATGATGATGATGAT 116
DB 71 TTTCTTGTGAGAGGCGGAGCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 130
QY 117 GGTAAACGATCGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 176
DB 131 GATTAATCTGGAAGACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 190
QY 177 GAAAGCTTTGGCTTTTGGAGCGGCGATGATGATGATGATGATGATGATGATGATGATGATGAT 236
DB 191 TTCGGGCTTTGGCTTTTGGAGCGGCGATGATGATGATGATGATGATGATGATGATGATGATGAT 250
QY 237 CTACCAAGGCGAGATCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 296
DB 251 TCACCTGAGCGAGATCTTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 310
QY 297 CACGGCCGAGCTCTTACCGGAGGAGCAGATGAGGGAATTTTGGACATGATGAGGCGCAAGCTT 356
DB 311 CACGGCCGAGCTCTTACCGGAGGAGCAGATGAGGGAATTTTGGACATGATGAGGCGCAAGCTT 370
QY 357 GATCAGCAATGCCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 416
DB 371 GATCAGCAATGCCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 430
QY 417 AAGAAAGGTTACGTAATTAATCGTGACTCATGACCGGATGATGATGATGATGATGATGATGATGAT 476
DB 431 AAGAAAGGTTACGTAATTAATCGTGACTCATGACCGGATGATGATGATGATGATGATGATGATGAT 490
QY 477 TAACTACGTGCGACAGAGCGCGGTATATCGTAGGTTGCAAGCGTTAATCGAATTAATCTG 536
DB 491 TAACTACGTGCGACAGAGCGCGGTATATCGTAGGTTGCAAGCGTTAATCGAATTAATCTG 550
QY 537 GCGTAAAGGTTGCGAGGCGCTTTGTAGTCAAGATGTAATCCCGGGCTTAACCTG 596
DB 551 GCGTAAAGGTTGCGAGGCGCTTTGTAGTCAAGATGTAATCCCGGGCTTAACCTG 610

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Oy 597 GAATGCGTTGAACCTACAGGCTAGATGTGGAGAGGAGGTGAATTCATGTGA 656
Db 611 GAATGCGATCTAAACTGTCAGCTAGACTCTTGTGAGAGGGAGTGAATTCATGTGA 670
Oy 657 GCAGTGAATGCGTGAAGATATGAAAGAACATCATGATGGGAAAGGACCTCTGGGTAA 716
Db 671 GCGGTGAATGCGTGAAGATATGAAAGAACATCATGATGGGAAAGGACCTCTGGGTAA 730
Oy 717 CACTGACGCTCATGACAGAAACCGTGGGAGAGAAACAGATTAATGATCCCTGTGTGCA 776
Db 731 GACTGACGCTCATGACAGAAACCGTGGGAGAGAAACAGATTAATGATCCCTGTGTGCA 790
Oy 777 GCACCTAAACAGATGCACTAGTGTGGGCTTATAGCTTGG-TAAAGAACTAAAG 835
Db 791 GCGGTGAATGCGTGAAGATATGAAAGAACATCATGATGGGAAAGGACCTCTGGGTAA 850
Oy 836 CGTGAAGTTGACCGGCTGGGAGTACGCTGCGAAGATTAAACCTCAAGAAATTGACGG 895
Db 851 CGTTAAATCGACCGCTGGGAGTACGCGCGCAAGTTAAATCTCAATGAATTGACGG 910
Oy 896 GACCGCGCAAGCGGTGATATGTGATTAATTCGATGCAACCGCAAAACCTTACTTA 955
Db 911 GCGCGCGCAAGCGGTGATATGTGATTAATTCGATGCAACCGCAAAACCTTACTTA 970
Oy 956 CCCTTGACATGATGAGCAATTTTCTAGAGATGATTAAGT-CCTTGGGAAACGTAACAG 1014
Db 971 CTCTTGACATGAGCAATTTTCTAGAGATGATTAAGT-CCTTGGGAAACGTAACAG 1030
Oy 1015 GTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1074
Db 1031 GTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1090
Oy 1075 GCACCCCTTGTATTAATTCGATGCA--TTTGTGGGCACTTAAATGAGTCCGCGT 1132
Db 1091 GCACCCCTTGTATTAATTCGATGCA--TTTGTGGGCACTTAAATGAGTCCGCGT 1150
Oy 1133 ACAACCGGAGAGAGGTGGGAGTGAAGTCAAGTCCCTGAGGCTTATGGGAGGCTTC 1192
Db 1151 ATTAACCGGAGAGAGGTGGGAGTGAAGTCAAGTCCCTGAGGCTTATGGGAGGCTTC 1210
Oy 1193 ACACGTATATACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1252
Db 1211 ACACGTGCTATACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1270
Oy 1253 AAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1312
Db 1271 AAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1330
Oy 1313 GTATTCGCGATGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1372
Db 1331 GTATTCGCGATGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1390
Oy 1373 CACACATGAGAGTGGTTCACAGAGAGAGTGAATCCGTAAGAGAGAGAGAGAGAGAG 1432
Db 1391 CACACATGAGAGTGGTTCACAGAGAGAGTGAATCCGTAAGAGAGAGAGAGAGAG 1450
Oy 1433 CACGCTGATTCATGACTGGGGTG 1457
Db 1451 CACTTGTGATTCATGACTGGGGTG 1475

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RESULT 12
US-10-831-286A-48671
; Sequence 48671, Application US/10831286A
; Publication No. US20060046246A1
; GENERAL INFORMATION:
; APPLICANT: ZENG, OIANDONG
; APPLICANT: CHATELIER, SONIA
; APPLICANT: MOIR, DONALD T.
; APPLICANT: LACROIX, BRUNA
; APPLICANT: CHILDRESS, DARRELL
; TITLE OF INVENTION: GENUS, GROUP, SPECIES AND/OR STRAIN SPECIFIC 16S rDNA SEQUENCES
; FILE REFERENCE: 032796-174.001

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; CURRENT APPLICATION NUMBER: US/10/831.286A
; CURRENT FILING DATE: 2004-04-25
; PRIOR APPLICATION NUMBER: 60/464,955
; PRIOR FILING DATE: 2003-04-24
; NUMBER OF SEQ ID NOS: 48788
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48671
; LENGTH: 1530
; TYPE: DNA
; ORGANISM: Citrobacter youngae
US-10-831-286A-48671

```

```

Query Match 69.2%; Score 1008.4; DB 9; Length 1530;
Best Local Similarity 82.4%; Pred. No. 2.6e-305;
Matches 1206; Conservative 0; Mismatches 251; Indels 7; Gaps 4;

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Oy 1 ATTGAACGCTGCGCGCATGCTTTACATGATGCAATGCAACGCGACGATGCTTG--- 57
Db 22 ATTGAACGCTGCGCGCATGCTTTACATGATGCAATGCAACGCGACGATGCTTG 81
Oy 58 -CATCTGCTGCGCATGCGCGCATGCTTTACATGATGCAATGCAACGCGACGATGCTTG 116
Db 82 TCCTTGGGTGACGATGCGCGCATGCTTTACATGATGCAATGCAACGCGACGATGCTTG 141
Oy 117 GGTAAACGATGCAAGATGCTTAAATCCGATTAATGCTTAAAGAGAGAGAGAGAGAGATC 176
Db 142 GATTAACGATGCAAGATGCTTAAATCCGATTAATGCTTAAAGAGAGAGAGAGAGATC 201
Oy 177 GAAAGACCTTGGCTTTTGGAGCGCGCATGCTTAAATGCTTAAAGAGAGAGAGAGATC 236
Db 202 TTGCGGCTTCTTGGCATGCTTAAATGCTTAAATGCTTAAAGAGAGAGAGAGATC 261
Oy 237 CTACCAAGGCGCATGATGATGCTTAAATGCTTAAATGCTTAAAGAGAGAGAGAGATC 296
Db 262 TCACCTAGGCGCATGATGCTTAAATGCTTAAATGCTTAAAGAGAGAGAGAGATC 321
Oy 297 CACGAGCGCATGCTTAAATGCTTAAATGCTTAAATGCTTAAAGAGAGAGAGAGATC 356
Db 322 CACGAGCGCATGCTTAAATGCTTAAATGCTTAAATGCTTAAAGAGAGAGAGAGATC 381
Oy 357 GATCAGCAATGCGCGCATGATGCTTAAATGCTTAAATGCTTAAAGAGAGAGAGAGATC 416
Db 382 GATCAGCAATGCGCGCATGATGCTTAAATGCTTAAATGCTTAAAGAGAGAGAGAGATC 441
Oy 417 AAGAAAGCTTAAATGCTTAAATGCTTAAATGCTTAAATGCTTAAAGAGAGAGAGAGATC 476
Db 442 AAGAAAGCTTAAATGCTTAAATGCTTAAATGCTTAAATGCTTAAAGAGAGAGAGAGATC 501
Oy 477 TAACTAGTGCAGACGCGCATGATGCTTAAATGCTTAAATGCTTAAAGAGAGAGAGATC 536
Db 502 TAACTAGTGCAGACGCGCATGATGCTTAAATGCTTAAATGCTTAAAGAGAGAGAGATC 561
Oy 537 GCGTAAAGGCTGCGCAGCGCGCTTAAATGCTTAAATGCTTAAAGAGAGAGAGAGATC 596
Db 562 GCGTAAAGGCTGCGCAGCGCGCTTAAATGCTTAAATGCTTAAAGAGAGAGAGAGATC 621
Oy 597 GAATGCGTTGAACCTACAGGCTAGTGTGCGAGAGAGAGAGAGAGAGAGAGAGATC 656
Db 622 GAATGCGTTGAACCTACAGGCTAGTGTGCGAGAGAGAGAGAGAGAGAGAGAGATC 681
Oy 657 GCAGTGAATGCGTGAAGATGATGAAGAAATGATGAGAGAGAGAGAGAGAGAGAGATC 716
Db 682 GCAGTGAATGCGTGAAGATGATGAAGAAATGATGAGAGAGAGAGAGAGAGAGAGATC 741
Oy 717 CACTGACGCTCATGACAGAAAGCGTGGGAGAGAGAGAGAGAGAGAGAGAGATC 776
Db 742 GACTGACGCTCATGACAGAAAGCGTGGGAGAGAGAGAGAGAGAGAGAGAGATC 801
Oy 777 GCGCTTAAAGAGATGCAATGCTTAAATGCTTAAATGCTTAAAGAGAGAGAGAGATC 835
Db 802 GCGCTTAAAGAGATGCAATGCTTAAATGCTTAAATGCTTAAAGAGAGAGAGAGATC 861
Oy 836 CGTGAAGTTGACCGCTGGGAGATGAGTGCAGAAATTAAATCAAGAAATTGACGG 895

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| Accession | Sequence  | Position |
|-----------|---|----------|
| QY        | ACCATGGAGATGGGGTTTACACAGAAAGCAGTAGTCTAACCGTAAAGAGGGGGCTTGCCAC | 1435     |
| QY        | 1376  |          |
| Db        | 1402  |          |
| Db        | 1402  |          |
| QY        | 1436  |          |
| QY        | 1462  |          |
| Db        | 1462  |          |

RESULT 15  
US-10-831

```

Sequence 48675, Application US/10831286A
Publication No. US20060046246A1
GENERAL INFORMATION:
APPLICANT: ZENG, QIANDONG
APPLICANT: CHATELIER, SONIA
APPLICANT: MOIR, DONALD T.
APPLICANT: LACROIX, BRUNA
APPLICANT: CHILDRESS, DARRELL
TITLE OF INVENTION: GENES, GROUP, SPECIES AND/OR STRAIN SPECIFIC 16S rDNA SEQUENCES
FILE REFERENCE: 032786-174.001
CURRENT APPLICATION NUMBER: US/10/831,286A
CURRENT FILING DATE: 2004-04-26
PRIOR APPLICATION NUMBER: 60/464,955
PRIOR FILING DATE: 2003-04-24
NUMBER OF SEQ ID NOS: 48788
SOFTWARE: PatentIn version 3.2
SEQ ID NO 48675
LENGTH: 1495
TYPE: DNA
ORGANISM: Proteus penneri
US-10-831-286A-48675

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|                       |              |                     |                 |                  |
|-----------------------|--------------|---------------------|-----------------|------------------|
| Query Match           | 69.0%;       | Score 1005.4;       | BD 9;           | Length 1495;     |
| Best Local Similarity | 82.7%;       | Pred. No. 2.3e-304; |                 |                  |
| Matches 121;          | Conservative | 0;                  | Mismatches 246; | Indels 8; Gaps 5 |

|    |     |   |     |
|----|-----|---|-----|
| Qy | 1   | ATTGAAGCGTGGCCGGCAGTCCTTACACATGCAAGTCGAAACGGCAGACAC--GGATCCTTGC   | 58  |
| Db | 1   | ATTGAAGCGTGGCCGGCAGGCCCTTAACACATGCAAGTCGAAACGGGTAAACAGAAAGAACTTGC | 60  |
| Qy | 59  | AT--CTGTGCGAGTGGCGGACGGGTGAGTAAATGCATCGAACGTATCCAGAAAGAGGG        | 116 |
| Db | 61  | TTTCTTGTGTGACGAGCGCGCGACGGGTGAGTAAATGATAGGGGATCTGCCGATAGAGGG      | 120 |
| Qy | 117 | GGTAACGATGAAAGATGTGTAAATACCGCATATCTTAAAGAGAGAAACGAGGGGATC         | 176 |
| Db | 121 | GATAACTACTGTAAGAAACGGTGGCTAAATACCGCATGACGCTTACGAGCAAAAGAGAGGGCTC  | 180 |
| Qy | 177 | GAAGACCTTGCCTTTTGGAGCGGCCGATGCTATTAAGTAGTAGTGGTGGGTAAAGGC         | 236 |
| Db | 181 | TTGGGACCTTGGCGTATCGAATGAACCCATAATGGATTAGTAGTAGAGTAGTAAAGGC        | 240 |
| Qy | 237 | CTACCAAGGCGACGATCAATGATGTTGTCAGAGAGACGACACGCACTAGGGACTGAGA        | 296 |
| Db | 241 | TCACCTAGGCGACCAATCTCTAGCTGGTCTGAGAGGATGATACGCAACTGGGACTTGAGA      | 300 |
| Qy | 297 | CACGAGCCAGACTCCTACGGGAGCAGACAGTAGGGGAAATTTTGGACAAATGGCGCAAGCCT    | 356 |
| Db | 301 | CACGGCCAGACTCCTACGGGAGGACAGACAGTAGGGGAAATTTTGCACAAATGGCGCAAGCCT   | 360 |
| Qy | 357 | GATCCAGCAATGCCCGCTGAAGTGAAGAGGCCCTTCGGGTTGTAAGCTCTTCACTCGAG       | 416 |
| Db | 361 | GATGCAGCCAGCCGCGCTGTATGAAGAGGCCCTTAGGGTTGTAAAGTACTTTCAACGGGG      | 420 |
| Qy | 417 | AAGAAAGGTATACGGTAAATATATCGTACTCATGACGCTATGACAGAAAGACACCGGC        | 476 |
| Db | 421 | AGAAAGGTATTAAGTTAATACCTTATCAATGACGTTACCCGCAAGAAAGACACCGGC         | 480 |
| Qy | 477 | TAATCTAGTGCAGAGACCCGCGGTAAATACGTAGGCTGCAAGGTTAAATCGAAATTAATCG     | 536 |
| Db | 481 | TAACTCGGTGCAGAGACCCGCGGTAAATACGGAGGGTGCACAGGTTAAATCGAAATTAATCG    | 540 |

|    |      |  |      |
|----|------|--|------|
| QY | 537  | GCCTAAAGCGGTGCGACGGCCGCTTTGTAAGTCAGATGTGAAATCCCGGGCTTAACTCTGG      | 536  |
| Dp | 541  | GCCTAAAGCGCACGGCGCGTCAATTAAAGTCAGATGTGAAACCCCGAGCTTAACTTGG         | 600  |
| QY | 597  | GAATTGCGTTTGAATCAACAGCTTGAATGTGGCAGAGGGAGGTGGAATTTCCATGTGTGA       | 656  |
| Dp | 601  | GAATTGCATCTGAAACCTGATTGGCTTAGAGTCTTTGATAGAGGGGGGTGAAATTTCCATGTGTGA | 660  |
| QY | 657  | GCAGTGAATGCGGTAGAGATATGTGAAGAAATCATGATGGCGAAGCGAGCCCTCTGGGTAA      | 716  |
| Dp | 661  | GGCGTGAATGCGGTAGAGATGTGAAGAAATCCGTTGGCGAAGCGGCCCTCTGGAGCAAA        | 720  |
| QY | 717  | CACGTACGCTCATGSCAGAAAGCGTGGGAGCAAAAGATTAATGATACCTCTGGTAGTCCA       | 776  |
| Dp | 721  | GACTGACGCTCAGGTGGGAAAGGTGGGAGAGCAAAACAGATTAATGATACCTCTGGTAGTCCA    | 780  |
| QY | 777  | CGCCCTAAACGATGTC-AACTAGTTGTGGGCTTATTAAGCTTGTGTAACGAAGCTAACG        | 835  |
| Dp | 781  | CGCTGTAAACGATGTGCAATTTAAGAGTTGTGGTCTTGAACCGGTGCTTGGAGCTAACG        | 840  |
| QY | 836  | CGTGAAGTTTACCGCCCTGGGGAGATTAAGTTCGCAAGATTAATCAAAAGGAATTGACGGG      | 895  |
| Dp | 841  | CGTTAAATTCACCGCTCGGGAGATACGGCCGCAAGGTTAAACTCAATATTAATTGACGGG       | 900  |
| QY | 896  | GACCCCGACAAAGCGGTGAGATTATGTGATTAATTCGATGCAACGCAAAAACCTTACCTTA      | 955  |
| Dp | 901  | GGCCCGACAAAGCGGTGAGCATGTGTGTTTAATTGATGCAAGCCGGAAGAACTTACCTTA       | 960  |
| QY | 956  | CCCTTGACATGTAGCCGAATTTCTTAGAGATAGTATAGTG-CTTGGGAACGCTTAACACAG      | 1014 |
| Dp | 961  | CTCTTGACATTCACGCGAATCTTTTAAGATAGAGAGAGTGCTTTCGGGAACGCTGAGACAG      | 1020 |
| QY | 1015 | GTCCTGATAGGCGTGTGTCAGCTCGTGTGTGAGATGGTGGGTTAAGTCCCGCAACGAGC        | 1074 |
| Dp | 1021 | GTGCTGATAGGCGTGTGTCAGCTCGTGTGTGAAATGTTGGTTAAGTCCCGCAACGAGC         | 1080 |
| QY | 1075 | GCAACCCCTTGTCATTAATTGCCATCATTTTG--GTTGGGCACTTTAAATGACACTGCCGTG     | 1132 |
| Dp | 1081 | GCAACCCCTTATCCTTTGTTGCCAGCCCGTGTATGGCCGGAACCTGAAGAGACCTGCCGTG      | 1140 |
| QY | 1133 | ACAAAACCGAGGAAGGTGGGGATGACGTCAAGTCTCATAGGCCCTTATGTGGTAGGGCTTC      | 1192 |
| Dp | 1141 | ATTAACCCGAGGAAGGTGGGGATGAGTCAAGTCAATCATATGAGCCCTTATACGATGGGCTAC    | 1200 |
| QY | 1193 | ACACGTATATCAATGTGCGGCTAATAGAGGGTTGGCAACCCCGAGGGGGAGGCTATCTCAG      | 1252 |
| Dp | 1201 | ACACGTGCTATCAATGTGCAATTAATAAGAAAGGACCTCGCGAGACCAACCGGAACCTCAT      | 1260 |
| QY | 1253 | AAAGCGGTGTATGTCGCCGATCGGAGTCTGCAACTCGAATCCGTTGAGAGTGGAAATCGCTTA    | 1312 |
| Dp | 1261 | AAAGTCTGTGTAGTCCGAGTTTGAATCTTGCACTGCACTCATGTAAGTGGAAATCGCTTA       | 1320 |
| QY | 1313 | GTAATCGCGGATCAGCATGTCCGGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGT       | 1372 |
| Dp | 1321 | GTAATCGGTATACGAATGTCTACGTAATAGCTTCCCGGGCTTGTACACACCGCCCGT          | 1380 |
| QY | 1373 | CACACCATGGGAGTGGGTTTACCAAGACAGGTATCTTAACCGTTAAGAGAGGGCGCTTGC       | 1432 |
| Dp | 1381 | CACACCATGGGAGTGGGTTTGCAAAAGAAAGTATAGTACTTAACTTTCGGGAGGGCGCTTAC     | 1440 |
| QY | 1433 | CACGGTGAAGTATGATGACTGGGGTG-1457                                    |      |
| Dp | 1441 | CACCTTGTGATTCATGACTGGGGTG-1465                                     |      |

Search completed: April 6, 2006, 21:46:35  
Job time : 731 secs





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 Qy 241 CAAGGCGAGATCAGTAGTGTCTGAGAGACGACACGCTGAGACTGAGACAG 300  
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 Db 361 CAGCAATGCGCGTGAAGTGAAGAGGCTTCCGGTTGTAAAGCTCTTTCAGTGAAGAGA 420  
 Qy 421 AAAGGTTACGGTAAATTAATGATGATCTCATGACGGTATCGACAGAAAGACCGGCTTAC 480  
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 Qy 481 TACGTCCAGACGCGCGGTAAATCGTAGGGGTGCAAGCTTAACTCGGAATTCGCGGCGT 540  
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 Db 721 GACGCTCATGCAAGAAAGCGTGGGAGCAAAACAGATTAGTAACTCCGTGTAGTCCAGCC 780  
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 Db 781 CTAAACGATGTCAACTAGTGTGGGCTTATTAAGCTTGTGTAACGAAAGCTTAACTGCTGA 840  
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 Qy 1381 GGGAGTGGGTTTCCACAGAGCAGGTAGTCTAACCTGAAGAGGCGCTTGGCAGCGTGA 1440  
 Db 1381 GGGAGTGGGTTTCCACAGAGCAGGTAGTCTAACCTGAAGAGGCGCTTGGCAGCGTGA 1440  
 Qy 1441 GATTCTGACTGGGGTG 1457  
 Db 1441 GATTCTGACTGGGGTG 1457  
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 US-10-659-980A-1  
 ; Sequence 1, Application US/10659980A  
 ; Publication No. US20040106133A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hovaneq, Timothy A  
 ; TITLE OF INVENTION: Method for Detecting Ammonia-Oxidizing Bacteria  
 ; FILE REFERENCE: 81289-284781  
 ; CURRENT APPLICATION NUMBER: US/10/659,980A  
 ; CURRENT FILING DATE: 2003-09-10  
 ; PRIOR APPLICATION NUMBER: US 09/573,684  
 ; PRIOR FILING DATE: 2000-05-19  
 ; PRIOR APPLICATION NUMBER: US 60/386,217  
 ; PRIOR FILING DATE: 2002-09-19  
 ; PRIOR APPLICATION NUMBER: US 60/386,218  
 ; PRIOR FILING DATE: 2002-09-19  
 ; PRIOR APPLICATION NUMBER: US 60/386,219  
 ; PRIOR FILING DATE: 2002-09-19  
 ; NUMBER OF SEQ ID NOS: 23  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 1  
 ; LENGTH: 1457  
 ; TYPE: DNA  
 ; ORGANISM: Unknown  
 ; OTHER INFORMATION: AOB Type A R7clone140 16S rDNA  
 US-10-659-980A-1  
 Query Match 100.0%; Score 1457; DB 7; Length 1457;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1457; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 Db 1 ATTTGAACGCTGGCGGCGATCTTTACATGACAGTGAACGCGCAGACGAGATCTTGCAAT 60  
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 Db 61 CTGTGGCGAGTGGCGGAGCGGCTGAGTAATGCAATGCGAAAGTATCCAGAAAGAGGGGGTA 120  
 Qy 121 AGGCATCGAAAGATGCTAATACCGCATATCTCTAAGAGAGAAAGCAGGGGATCGAAA 180  
 Db 121 AGGCATCGAAAGATGCTAATACCGCATATCTCTAAGAGAGAAAGCAGGGGATCGAAA 180  
 Qy 181 GACCTTGCCTTTTGGAGCGGCGGATGTCTGATTAGCTAGTTGGTGGGTTAAAGGCTTAC 240  
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 Db 301 GCCCAGACTCTTACCGGAGGAGCAGAGTGGGAAATTTTGGACATGGGCGCAAGCTGATC 360  
 Qy 361 CAGCAATGCGCGGTGAGTGAAGAGGCTTCCGGTTGTAAAGCTCTTTCAGTGAAGAGA 420  
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421 AAAGTTACGGTAATAATCTGACTCATGACGGTATGACAGAAAGACACCGGCTTAC 480  
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 841 AGTTGACCGGCTGGGAGTACCGTGGCAAGATTAACTCAAGAAATTGACGGGAGCC 900  
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 1141 GAGGAAGGTGGGATGACGTCAGATCTTCATGAGGCTTATGAGGAGGCTTACACGTA 1200  
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 1321 GGATCAGCATGTGCGGTGAATACGTTCCGGGTCTTGTACACACCGCCGCTCAACCAT 1380  
 1381 GGGAGTGGTTTCAACAGAGAGTGTCTAATCCGTAAAGAGGAGGCGCTTGCACAGGTGA 1440  
 1381 GGGAGTGGTTTCAACAGAGAGTGTCTAATCCGTAAAGAGGAGGCGCTTGCACAGGTGA 1440  
 1441 GATTTCATGCTGGGGTG 1457  
 1441 GATTTCATGCTGGGGTG 1457

RESULT 3  
 US-10-659-983A-1  
 ; Sequence 1, Application US/10659983A  
 ; Publication No. US20040157313A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hovaneq, Timothy A  
 ; TITLE OF INVENTION: Ammonia-Oxidizing Bacteria  
 ; FILE REFERENCE: 81289-28479  
 ; CURRENT APPLICATION NUMBER: US/10/659, 983A  
 ; PRIOR FILING DATE: 2003-09-10  
 ; PRIOR APPLICATION NUMBER: US 09/573,684  
 ; PRIOR FILING DATE: 2000-05-19  
 ; PRIOR APPLICATION NUMBER: US 60/386,217  
 ; PRIOR FILING DATE: 2002-09-19  
 ; PRIOR APPLICATION NUMBER: US 60/386,218  
 ; PRIOR FILING DATE: 2002-09-19  
 ; PRIOR APPLICATION NUMBER: US 60/386,219  
 ; PRIOR FILING DATE: 2002-09-19  
 ; NUMBER OF SEQ ID NOS: 23  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 1  
 ; LENGTH: 1457  
 ; TYPE: DNA  
 ; ORGANISM: Unknown  
 ; FEATURE:  
 ; OTHER INFORMATION: MOB Type A R7clonel40 16S rDNA  
 US-10-659-983A-1  
 Query Match 100.0%; Score 1457; DB 7; Length 1457;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1457; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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 1 ATTGAACGCTGGCGCATGCTTTACATGCAAGTTCGACCGCAGCAGATGCTTGCAT 60  
 61 CTGTGGCGAGTGGCGGACCGGTGAGTAATCCATCCGAAAGCTATCCAGAGGGGGGTA 120  
 61 CTGTGGCGAGTGGCGGACCGGTGAGTAATCCATCCGAAAGCTATCCAGAGGGGGGTA 120  
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 541 AAAGGTCGACAGCGGCTTTGTAAGTCAAGTGTAAATCCCGGCTTAACTGGGAAT 600

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QY 601 TGGCTTGAACCTACAGGCTAGAGTGGCGAGGAGGAGGTAATTCATGCTACAG 660
DB 601 TGGCTTGAACCTACAGGCTAGAGTGGCGAGGAGGAGGTAATTCATGCTACAG 660
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DB 661 TGAATGCGTAGAGATATGAGAAACATCGATGGCGAGGAGGCTCTGGGTTAACT 720
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DB 721 GAGCGCTATGCAAGAAAGCGTGGGAGCAACAGATTAATACCTGTGATCCAGCC 780
QY 781 CTAAAGCATGCACTAGTGTGGGCTTATAGGCTGTGTAACGAGCTAACGGGTGA 840
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DB 841 AGTTGACCCGCTGGGAGTACGCTCGCAAGATTAACTCAAGAAATTAACGGGAGCC 900
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DB 1141 GAGGAGGTGGGATGACGCTCAAGTCTCAATGCGCTTATGGGAGGCTTCAACAGTAA 1200
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DB 1201 TACAAATGCGCGCTACAGAGGTTGCCAACCCGCGAGGAGGAGCTAATCTGAGAAAGCGC 1260
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QY 1381 GGGAGTGGGTTTACAGAGAGAGAGTGTAAACCGTAAGAGAGGCGCTTCCACGCTGA 1440
DB 1381 GGGAGTGGGTTTACAGAGAGAGAGTGTAAACCGTAAGAGAGGCGCTTCCACGCTGA 1440
QY 1441 GATTCACTGAGGAGTG 1457
DB 1441 GATTCACTGAGGAGTG 1457

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RESULT 4
US-10-659-948a-2
; Sequence 2, Application US/10659948A
; Publication No. US20040101946A1
; GENERAL INFORMATION:
; APPLICANT: Hovance, Timothy A
; TITLE OF INVENTION: Method of Using Ammonia-Oxidizing Bacteria
; FILE REFERENCE: 81289-294309
; CURRENT APPLICATION NUMBER: US/10/659, 948A
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: US 09/573, 684
; PRIOR FILING DATE: 2000-05-19

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; PRIOR APPLICATION NUMBER: US 60/386,217
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,218
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,219
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patent version 3.2
; SEQ ID NO 2
; LENGTH: 1457
; TYPE: DNA
; ORGANISM: Unknown
; OTHER INFORMATION: AOB Type A1 R7clone187 16S rDNA
US-10-659-948a-2

Query Match 99.7%; Score 1452.2; DB 7; Length 1457;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1454; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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DB 121 AGCATCGAAAGATGCTAATATCCGATATATCTTAAGAGAGAAAGCAGGGATGAAA 180
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DB 721 GAGCGCTATGCAAGAAAGCGTGGGAGCAACAGATTAATACCTGTGATCCAGCC 780
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Db      841 AGTTGACCGCTGGGAGTACGCTGCAAGATTAACTCAAGGAATTGACGGGACCC 900
Qy      901 GCACAGCGGTGATTAATGATTAATTCATGCAAGCGGAAAACTTACCTTACCCTT 960
Db      901 GCACAGCGGTGATTAATGATTAATTCATGCAAGCGGAAAACTTACCTTACCCTT 960
Qy      961 GACATGTAGCAATTTTCTAGAGATAGATTAGTCTGGGAAAGCTTACACAGGTGCTG 1020
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Qy      1021 CATGGCTGTCTGACGCTGTCTGAGATGTTGGGTTAAGTCCGCAACGACGCAAC 1080
Db      1021 CATGGCTGTCTGACGCTGTCTGAGATGTTGGGTTAAGTCCGCAACGACGCAAC 1080
Qy      1081 CTTGTCAATTAATTCATCACTTTTGGTGGGCACTTTAATGAGACTGCGGTTGACAA 1140
Db      1081 CTTGTCAATTAATTCATCACTTTTGGTGGGCACTTTAATGAGACTGCGGTTGACAA 1140
Qy      1141 GAGGAGGTGGGAGATGAGTCAAGTCTCATGAGCCCTTATGGGTGGGCTTACACGTA 1200
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Qy      1261 TCGTAGTCCGATCGGAGTCTGCAACTGACTCCGCTGAAGTGGAAATGCTAATGAT 1320
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Qy      1321 GGATCAGCATGTCGCGGTGAAATAGCTTCCGGGCTTTGTACACACCGCCCTCAACAT 1380
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Qy      1381 GGGAGTGGGTTTCAACAGAGAGGTAGTCTAACCGTAAGAGAGGCGCTTGGCAAGTGA 1440
Db      1381 GGGAGTGGGTTTCAACAGAGAGGTAGTCTAACCGTAAGAGAGGCGCTTGGCAAGTGA 1440
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RESULT 5  
US-10-659-980A-2

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; Sequence 2, Application US/10659980A
; Publication No. US20040106133A1
; GENERAL INFORMATION:
; APPLICANT: Hovanec, Timothy A
; TITLE OF INVENTION: Method for Detecting Ammonia-Oxidizing Bacteria
; FILE REFERENCE: 81289-284781
; CURRENT APPLICATION NUMBER: US/10/659,980A
; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: US 09/573,684
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 60/386,217
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,218
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,219
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 1457
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:

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OTHER INFORMATION: AOB Type A1 R7clone187 16S rDNA  
US-10-659-980A-2

Query Match 99.74; Score 1452.2; DB 7; Length 1457;  
Best Local Similarity 99.88; Pred. No. 0;  
Matches 1454; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy      1 ATTGAAGCTGGGGGCAATGCTTTACATGATGCAATGCAAGCGGACGAGTGTGTCAT 60
Db      1 ATTGAAGCTGGGGGCAATGCTTTACATGATGCAATGCAAGCGGACGAGTGTGTCAT 60
Qy      61 CTGTGGCGAGTGGCGGACGCGGTGATGATGCAATGCAATGCAATGCAATGCAATGCA 120
Db      61 CTGTGGCGAGTGGCGGACGCGGTGATGATGCAATGCAATGCAATGCAATGCAATGCA 120
Qy      121 ACGCATGCAAGATGTGCTAATACCGCATATCTCTAAGAGAAAGCAAGGAGATCGAAA 180
Db      121 ACGCATGCAAGATGTGCTAATACCGCATATCTCTAAGAGAAAGCAAGGAGATCGAAA 180
Qy      181 GACCTTGCGCTTTGGAGCGGCGGATGCTGATTAAGTGTGGGTAAAGGCTTAC 240
Db      181 GACCTTGCGCTTTGGAGCGGCGGATGCTGATTAAGTGTGGGTAAAGGCTTAC 240
Qy      241 CAAGCGACGATCAGTATGTTGCTGAGAGGACGACGACGACGACGACGACGACGACG 300
Db      241 CAAGCGACGATCAGTATGTTGCTGAGAGGACGACGACGACGACGACGACGACGACG 300
Qy      301 GCCAGACTCTTACGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
Db      301 GCCAGACTCTTACGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 360
Qy      361 CAGCAATGCGCGGTGAGTGAAGAGGCTTGGGTTGAAGCTTCACTCGAAGAA 420
Db      361 CAGCAATGCGCGGTGAGTGAAGAGGCTTGGGTTGAAGCTTCACTCGAAGAA 420
Qy      421 AAAGTTACGCTTAATATATCTGATCATGACGCTATGACAGAGAAAGCAACCGCTAAC 480
Db      421 AAAGTTACGCTTAATATATCTGATCATGACGCTATGACAGAGAAAGCAACCGCTAAC 480
Qy      481 TAGGTGCCAGAGCGCGGCTAATACGTAAGGTTGCAAGCGCTTAATCGGAATTAC 540
Db      481 TAGGTGCCAGAGCGCGGCTAATACGTAAGGTTGCAAGCGCTTAATCGGAATTAC 540
Qy      541 AAAGGTGCGGAGCGGCTTTGTAACTGATGCAATGCAATGCAATGCAATGCAATGCA 600
Db      541 AAAGGTGCGGAGCGGCTTTGTAACTGATGCAATGCAATGCAATGCAATGCAATGCA 600
Qy      601 TGGCTTTGAATCTAAGGCTAGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
Db      601 TGGCTTTGAATCTAAGGCTAGAGTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 660
Qy      661 TGAATGCTAGATATGGAAGAACTGATGCGAAGGAGGAGGAGGAGGAGGAGGAGGAG 720
Db      661 TGAATGCTAGATATGGAAGAACTGATGCGAAGGAGGAGGAGGAGGAGGAGGAGGAG 720
Qy      721 GACGCTATGCAAGAAAGCGTGGGAGCAAAACAGATTAAATCCCTGCTGATGCAAGCC 780
Db      721 GACGCTATGCAAGAAAGCGTGGGAGCAAAACAGATTAAATCCCTGCTGATGCAAGCC 780
Qy      781 CTAACGATGCACTAGTGTGGGCTTATTAAGGCTTGTGTAAGCAAGCTAACGCGTGA 840
Db      781 CTAACGATGCACTAGTGTGGGCTTATTAAGGCTTGTGTAAGCAAGCTAACGCGTGA 840
Qy      841 AGTTGACCGCTGGGAGTACGCTGCAAGATTAACTCAAGGAATTGACGGGACCC 900
Db      841 AGTTGACCGCTGGGAGTACGCTGCAAGATTAACTCAAGGAATTGACGGGACCC 900
Qy      901 GCACAGCGGTGATTAATGATTAATTCATGCAAGCGGAAAACTTACCTTACCCTT 960
Db      901 GCACAGCGGTGATTAATGATTAATTCATGCAAGCGGAAAACTTACCTTACCCTT 960
Qy      961 GACATGTAGCAATTTTCTAGAGATAGATTAGTCTGGGAAAGCTTACACAGGTGCTG 1020

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Db 961 GACATGAGCGAATTTCTAGATAGATTAGTCTTGGGAAAGCTAACAAGAGTCTG 1020  
 Qy 1021 CAGGCTGTGTCAAGCTCTGTGTGTGATGTTAGTTAGTCCCGAAGAGCGCAAC 1080  
 Db 1021 CAGGCTGTGTCAAGCTCTGTGTGTGATGTTAGTTAGTCCCGAAGAGCGCAAC 1080  
 Qy 1081 CTGTGATTAATTAATGATCAATTTGTTGGGCACTTTAATGAGACTGCGGTGACAAACG 1140  
 Db 1081 CTGTGATTAATTAATGATCAATTTGTTGGGCACTTTAATGAGACTGCGGTGACAAACG 1140  
 Qy 1141 GAGGAAGTGGGAGATGACGTCAAGTCTCAATGAGCCCTTAATGGGTAGGGCTTCAACGTAA 1200  
 Db 1141 GAGGAAGTGGGAGATGACGTCAAGTCTCAATGAGCCCTTAATGGGTAGGGCTTCAACGTAA 1200  
 Qy 1201 TACAAATGGCGGCTACAGAGGTTGGCCACCCCGAGAGGGAGAGCTAATCTCAAGAAAGCGG 1260  
 Db 1201 TACAAATGGCGGCTACAGAGGTTGGCCACCCCGAGAGGGAGAGCTAATCTCAAGAAAGCGG 1260  
 Qy 1261 TCGTAGTCCGATCGAGACTGCAACTGCACTCCGTAAGTGGAAATCGTAGTAATCGC 1320  
 Db 1261 TCGTAGTCCGATCGAGACTGCAACTGCACTCCGTAAGTGGAAATCGTAGTAATCGC 1320  
 Qy 1321 GATCAAGCATGTGCGGTGAATAGTTCCTCGGTCTTTGACACACCGCCCTGACACCAT 1380  
 Db 1321 GATCAAGCATGTGCGGTGAATAGTTCCTCGGTCTTTGACACACCGCCCTGACACCAT 1380  
 Qy 1381 GGGAGTGGGTTTACCAAGAGAGGTAGTCTAACCGTAAGAGGCGCTTCCACCGGTGA 1440  
 Db 1381 GGGAGTGGGTTTACCAAGAGAGGTAGTCTAACCGTAAGAGGCGCTTCCACCGGTGA 1440  
 Qy 1441 GATTCACTGAGTGGGTG 1457  
 Db 1441 GATTCACTGAGTGGGTG 1457

## RESULT 6

US-10-659-983A-2

Sequence 2: Application US/10659983A

Publication No. US2004015731A1

GENERAL INFORMATION:

APPLICANT: Hovane, Timothy A

TITLE OF INVENTION: Ammonia-Oxidizing Bacteria

FILE REFERENCE: 81289-284779

CURRENT APPLICATION NUMBER: US/10/659,983A

CURRENT FILING DATE: 2003-09-10

PRIOR APPLICATION NUMBER: US 09/573,684

PRIOR FILING DATE: 2000-05-19

PRIOR APPLICATION NUMBER: US 60/386,217

PRIOR FILING DATE: 2002-09-19

PRIOR APPLICATION NUMBER: US 60/386,218

PRIOR FILING DATE: 2002-09-19

PRIOR APPLICATION NUMBER: US 60/386,219

PRIOR FILING DATE: 2002-09-19

NUMBER OF SEQ ID NOS: 23

SOFTWARE: Patent version 3.2

SEQ ID NO 2

LENGTH: 1457

TYPE: DNA

ORGANISM: Unknown

FEATURE:

OTHER INFORMATION: AOB Type A1 R7clone187 16S rDNA

US-10-659-983A-2

Query Match 99.7%; Score 1452.2; DB 7; Length 1457;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 1454; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATTGAACGCTGGGCGGATGCTTTACATGCAAGTGCAGCGGAGCGAGATGCTTCAT 60  
 Db 1 ATTGAACGCTGGGCGGATGCTTTACATGCAAGTGCAGCGGAGCGAGATGCTTCAT 60  
 Qy 61 CTGTGCGGAGTGGCGGAGCGGTGAGTAAATGATCGGAAGCTATCCAGAAAGAGGGGGTGA 120  
 Db 61 CTGTGCGGAGTGGCGGAGCGGTGAGTAAATGATCGGAAGCTATCCAGAAAGAGGGGGTGA 120

Db 61 CTGTGCGGAGTGGCGGAGCGGTGAGTAAATGATCGGAAGCTATCCAGAAAGAGGGGGTGA 120  
 Qy 121 AGCATCGAAGATGCTTAATACCGCATATCTCTAAGAGAGAAAGACAGGGGATCGAAA 180  
 Db 121 AGCATCGAAGATGCTTAATACCGCATATCTCTAAGAGAGAAAGACAGGGGATCGAAA 180  
 Qy 181 GACCTTGCCCTTTTGGAGCGGCGATGCTGATTAAGTACTAGTTGGTGGGTTAAAGGCTTAC 240  
 Db 181 GACCTTGCCCTTTTGGAGCGGCGATGCTGATTAAGTACTAGTTGGTGGGTTAAAGGCTTAC 240  
 Qy 241 CAAAGCGAGATCAGTAGTTGGTCTGAGAGAGACAGACACCTGCGGACTGAGACAG 300  
 Db 241 CAAAGCGAGATCAGTAGTTGGTCTGAGAGAGACAGACACCTGCGGACTGAGACAG 300  
 Qy 301 GCCCAACCTCTAAGGAGAGCGAGCTGGGGAATTTTGGACATGGGCGCAAGCCGTATC 360  
 Db 301 GCCCAACCTCTAAGGAGAGCGAGCTGGGGAATTTTGGACATGGGCGCAAGCCGTATC 360  
 Qy 361 CAGCAATGCGCGGTGAGTGAAGAGGCTTGGGTTGTAAAGTCTTTTCAAGTCGAGAGA 420  
 Db 361 CAGCAATGCGCGGTGAGTGAAGAGGCTTGGGTTGTAAAGTCTTTTCAAGTCGAGAGA 420  
 Qy 421 AAAGTTACGTTAATATCTGATCTCATGACGGTATCGACAGAGAAAGACCGGCTAAC 480  
 Db 421 AAAGTTACGTTAATATCTGATCTCATGACGGTATCGACAGAGAAAGACCGGCTAAC 480  
 Qy 481 TACGTGCGAGACGCGCGGTAAATAGTAGGAGCAAGCTTAATCGGAATTAATCGGAGCT 540  
 Db 481 TACGTGCGAGACGCGCGGTAAATAGTAGGAGCAAGCTTAATCGGAATTAATCGGAGCT 540  
 Qy 541 AAAGGTGCGAGGCGGCTTTGTAAAGTCAGATGTGAAATCCCGGGCTTAACTGAGGAAT 600  
 Db 541 AAAGGTGCGAGGCGGCTTTGTAAAGTCAGATGTGAAATCCCGGGCTTAACTGAGGAAT 600  
 Qy 601 TCGCTTTAACTCAAGGCTAAGTGTGCGAGAGGAGAGTGAATTCATGTGTAGCAG 660  
 Db 601 TCGCTTTAACTCAAGGCTAAGTGTGCGAGAGGAGAGTGAATTCATGTGTAGCAG 660  
 Qy 661 TGAATGCGTAGAATATGGAAGAAATCATGATGGGGAAGAGGCGCTTGGGTTAACT 720  
 Db 661 TGAATGCGTAGAATATGGAAGAAATCATGATGGGGAAGAGGCGCTTGGGTTAACT 720  
 Qy 721 GACGCTCATGACAGAAAGCGTGGGAGCAAGAGATTAAGTACCTGTAGTCCAGCGC 780  
 Db 721 GACGCTCATGACAGAAAGCGTGGGAGCAAGAGATTAAGTACCTGTAGTCCAGCGC 780  
 Qy 781 CTAAACGATGCACTAGTTGTTGGGCTTATTAAGGCTTGTGAACGACCTAACCGGTGA 840  
 Db 781 CTAAACGATGCACTAGTTGTTGGGCTTATTAAGGCTTGTGAACGACCTAACCGGTGA 840  
 Qy 841 AGTTGACCGGCTGGGAGAGTGGTGGCAAGATTTAAACCAAGGAATTGACGGGAGACC 900  
 Db 841 AGTTGACCGGCTGGGAGAGTGGTGGCAAGATTTAAACCAAGGAATTGACGGGAGACC 900  
 Qy 901 GCACAAGCGGTGATTAATGATTAATTCGATGCAAGCGCAAAAACCTTACTCACTT 960  
 Db 901 GCACAAGCGGTGATTAATGATTAATTCGATGCAAGCGCAAAAACCTTACTCACTT 960  
 Qy 961 GACATGTAAGCAATTTTCTAGAGATGATTAAGTCTTGGGAAACCTTAACAGAGTGTG 1020  
 Db 961 GACATGTAAGCAATTTTCTAGAGATGATTAAGTCTTGGGAAACCTTAACAGAGTGTG 1020  
 Qy 1021 CAGGCTGTGTCAAGCTCTGTGTGTGATGTTAGTTAGTCCCGAAGAGCGCAAC 1080  
 Db 1021 CAGGCTGTGTCAAGCTCTGTGTGTGATGTTAGTTAGTCCCGAAGAGCGCAAC 1080  
 Qy 1081 CTGTGATTAATTAATGATCAATTTGTTGGGCACTTTAATGAGACTGCGGTGACAAACG 1140  
 Db 1081 CTGTGATTAATTAATGATCAATTTGTTGGGCACTTTAATGAGACTGCGGTGACAAACG 1140  
 Qy 1141 GAGGAAGTGGGAGATGACGTCAAGTCTCAATGAGCCCTTAATGGGTAGGGCTTCAACGTAA 1200  
 Db 1141 GAGGAAGTGGGAGATGACGTCAAGTCTCAATGAGCCCTTAATGGGTAGGGCTTCAACGTAA 1200

QY 1201 TACATGCGCGTACAGAGGTTGCCAACCCCGGAGGAGCTTAATCTCAGAAAGCCG 1260  
DB 1201 TACAAATGCGCGGTACAGAGGTTGCCAACCCCGGAGGAGCTTAATCTCAGAAAGCCG 1260  
QY 1261 TCGTAGTCCGAGTGGAGTCTGCAACTGACCTCCGAGTGAAGTCGGAATGCTAGTAATGCG 1320  
DB 1261 TCGTAGTCCGAGTGGAGTCTGCAACTGACCTCCGAGTGAAGTCGGAATGCTAGTAATGCG 1320  
QY 1321 GGATCAGCATGTCCGCGTGAATACGTTCCCGGCTCTTGTACACACCCGCGCTCACCAT 1380  
DB 1321 GGATCAGCATGTCCGCGTGAATACGTTCCCGGCTCTTGTACACACCCGCGCTCACCAT 1380  
QY 1381 GGGAGTGGCTTTCACAGAGAGAGTACTCTAACCTGAAGAGGCGCTTGCACAGTGA 1440  
DB 1381 GGGAGTGGCTTTCACAGAGAGAGTACTCTAACCTGAAGAGGCGCTTGCACAGTGA 1440  
QY 1441 GATTCAATGACTGGGGTG 1457  
DB 1441 GATTCAATGACTGGGGTG 1457

RESULT 7  
US-10-659-948A-20  
Sequence 20, Application US/10659948A  
Publication No. US20040101946A1  
GENERAL INFORMATION:  
APPLICANT: Hovaneq, Timothy A  
TITLE OF INVENTION: Method of Using Ammonia-Oxidizing Bacteria  
FILE REFERENCE: 81289-294309  
CURRENT APPLICATION NUMBER: US/10/659,948A  
CURRENT FILING DATE: 2003-09-10  
PRIOR APPLICATION NUMBER: US 09/573,684  
PRIOR FILING DATE: 2000-05-19  
PRIOR APPLICATION NUMBER: US 60/386,217  
PRIOR FILING DATE: 2002-09-19  
PRIOR APPLICATION NUMBER: US 60/386,218  
PRIOR FILING DATE: 2002-09-19  
PRIOR APPLICATION NUMBER: US 60/386,219  
PRIOR FILING DATE: 2002-09-19  
NUMBER OF SEQ ID NOS: 23  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 20  
LENGTH: 1491  
TYPE: DNA  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: N. Aestuarii-like AOB B16clone57 16S rDNA  
US-10-659-948A-20

Query Match 95.5%; Score 1391.6; DB 7; Length 1491;  
Best Local Similarity 97.6%; Pred. No. 0;  
Matches 1423; Conservative 0; Mismatches 34; Indels 1; Gaps 1;

QY 301 GCCCAGACTCCTACGGGAGGACAGCAGTGGGAAATTTTGAACAATGGGCGCAAGCCTGATC 360  
DB 318 GCCCAGACTCCTACGGGAGGACAGCAGTGGGAAATTTTGAACAATGGGCGCAAGCCTGATC 377  
QY 361 CAGCAATGCGCGGTAGTGAAGAGGCTTCCGGTTGTAAAGCTCTTCACTGAGAGA 420  
DB 378 CAGCAATGCGCGGTAGTGAAGAGGCTTCCGGTTGTAAAGCTCTTCACTGAGAGA 437  
QY 421 AAGGTTACGGTAATATATGTAATCTATGACGGTATGACAGAGAGAGCACCCTTAC 480  
DB 438 AAGGTTACGGTAATATATGTAATCTATGACGGTATGACAGAGAGAGCACCCTTAC 497  
QY 481 TAGCTGCACAGCGCGGTAAATACGTAAGGTTGCAAGCTTAAATCGAATTTACTGGCGT 540  
DB 498 TAGCTGCACAGCGCGGTAAATACGTAAGGTTGCAAGCTTAAATCGAATTTACTGGCGT 557  
QY 541 AAGGTTGCGCAGCGCGCTTGTAACTAGTGAATGAAATCCCGGGCTTAACTGGAGAT 600  
DB 558 AAGGTTGCGCAGCGCGCTTGTAACTAGTGAATGAAATCCCGGGCTTAACTGGAGAT 617  
QY 601 TCGTTTGAATCTAACAGGCTAGAGTGCAGAGAGGAGTGAATTCATGTAGCAG 660  
DB 618 TCGTTTGAATCTAACAGGCTAGAGTGCAGAGAGGAGTGAATTCATGTAGCAG 677  
QY 661 TGAATGCGTGAAGATTTGGAAGAACTGATGGCGGAAGCAGCTCTGGGTTAACT 720  
DB 678 TGAATGCGTGAAGATTTGGAAGAACTGATGGCGGAAGCAGCTCTGGGTTAACT 737  
QY 721 GAGGCTATGACAGAAAGCGTGGGAGCAAAACAGATTAAGTACCTGTAGTCCAGCC 780  
DB 738 GAGGCTATGACAGAAAGCGTGGGAGCAAAACAGATTAAGTACCTGTAGTCCAGCC 797  
QY 781 CTAAACAGATGCAACTAGTGTGGGCTTATTAAGCTTGTGTAACGAAGTAACTGCGTGA 840  
DB 798 CTAAACAGATGCAACTAGTGTGGGCTTATTAAGCTTGTGTAACGAAGTAACTGCGTGA 857  
QY 841 AGTTGACCGGCTGGGAGTACCGTGCAGAAATTTAACTGAAGGAAATTAAGCGGGAGCC 900  
DB 858 AGTTGACCGGCTGGGAGTACCGTGCAGAAATTTAACTGAAGGAAATTAAGCGGGAGCC 917  
QY 901 GCACAGCGGTGATTAATGATGATTAATTCATGCAACGCGAAACCTTAACTTACCTT 960  
DB 918 GCACAGCGGTGATTAATGATGATTAATTCATGCAACGCGAAACCTTAACTTACCTT 977  
QY 961 GACATGAGCGAATTTCTAGATGATTAATTCATGCAACGCGT 1019  
DB 978 GACATGAGCGAATTTCTAGATGATTAATTCATGCAACGCGT 1037  
QY 1020 GCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1079  
DB 1038 GCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1097  
QY 1080 CTTGTGATTAATTCATGATTAATTCATGATTAATTCATGATTAATTCATGATTAATTCAT 1139  
DB 1098 CTTGTGATTAATTCATGATTAATTCATGATTAATTCATGATTAATTCATGATTAATTCAT 1157  
QY 1140 GAGAGAGTGGGAGTACGCTCAAGTCTCATGCGCTTATGAGTGGTGAAGCTTCAACGTA 1199  
DB 1158 GAGAGAGTGGGAGTACGCTCAAGTCTCATGCGCTTATGAGTGGTGAAGCTTCAACGTA 1217  
QY 1200 ATACATAGCGCGTACAGAGGTTGCAACCCGAGAGGAGGAGTAACTTCAAGAAAGCCG 1259  
DB 1218 ATACATAGCGCGTACAGAGGTTGCAACCCGAGAGGAGGAGTAACTTCAAGAAAGCCG 1277  
QY 1260 GTCTAGTCCGAGTGGAGTCTGCAACTCCGTAAGTGGAGTGGAGTGGAGTGGAGTGGAGT 1319  
DB 1278 GTCTAGTCCGAGTGGAGTCTGCAACTCCGTAAGTGGAGTGGAGTGGAGTGGAGTGGAGT 1337  
QY 1320 CGGATCAGATGTCGCGGTAAATACGTTCCCGGCTTGTACACACCGCGCTACACCA 1379  
DB 1338 CGGATCAGATGTCGCGGTAAATACGTTCCCGGCTTGTACACACCGCGCTACACCA 1397

QY 1380 TGGAGTGGGTTTCCACGAGAGCATGATCTAACCGTAAAGAGGGCGTTGCCACGGTG 1439  
 DB 1398 TGGAGTGGGTTTCCACGAGAGCATGATCTAACCGTAAAGAGGGCGTTGCCACGGTG 1457  
 QY 1440 AGATTCACTGAGGGGTG 1457  
 DB 1458 AGATTCACTGAGGGGTG 1475

## RESULT 8

US-10-659-980A-20  
 ; Sequence 20, Application US/10659980A  
 ; Publication No. US20040106133A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hovane, Timothy A  
 ; TITLE OF INVENTION: Method for Detecting Ammonia-Oxidizing Bacteria  
 ; FILE REFERENCE: 81289-284781  
 ; CURRENT APPLICATION NUMBER: US/10/659,980A  
 ; CURRENT FILING DATE: 2003-09-10  
 ; PRIOR APPLICATION NUMBER: US 09/573,684  
 ; PRIOR FILING DATE: 2000-05-19  
 ; PRIOR APPLICATION NUMBER: US 60/386,217  
 ; PRIOR FILING DATE: 2002-09-19  
 ; PRIOR APPLICATION NUMBER: US 60/386,218  
 ; PRIOR FILING DATE: 2002-09-19  
 ; PRIOR APPLICATION NUMBER: US 60/386,219  
 ; PRIOR FILING DATE: 2002-09-19  
 ; NUMBER OF SEQ ID NOS: 23  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 20  
 ; LENGTH: 1491  
 ; TYPE: DNA  
 ; ORGANISM: Unknown  
 ; FEATURE:  
 ; OTHER INFORMATION: N. Aestuarii-like AOB Bp16clones57 16S rDNA  
 US-10-659-980A-20

Query Match 95.5%; Score 1391.6; DB 7; Length 1491;  
 Best Local Similarity 97.6%; Pred. No. 0;  
 Matches 1423; Conservative 0; Mismatches 34; Indels 1; Gaps 1;

QY 1 ATGGAACGCTGGCGGCGATGCTTTACACATGCAAGTCCGAACGGGAGCGATGCTGCAT 60  
 DB 18 ATTGAACGCTGGCGGCGATGCTTTACACATGCAAGTCCGAACGGGAGCGATGCTGCAC 77  
 QY 61 CTGTGGCGAGTGGCGGAGCGGTGATGATGCAATCGGAACGTATCCGAAGAGGGGGTGA 120  
 DB 78 CTGTGGCGAGTGGCGGAGCGGTGATGATGCAATCGGAACGTATCCGAAGAGGGGGTGA 137  
 QY 121 ACGCATGGAAGATGCTTAATACCGCATATTACTTAAGAGGAAAGACGGGATCGAAA 180  
 DB 138 ACCCATGGAAGATGCTTAATACCGCATATTACTTAAGAGGAAAGACGGGATCGAAA 197  
 QY 181 GACCTTGCGCTTTTGAAGCGGCGATGCTGATTAGTAGTGGTGAAGGCGCTAC 240  
 DB 198 GACCTTGCGCTTTTGAAGCGGCGATGCTGATTAGTAGTGGTGAAGGCGCTAC 257  
 QY 241 CAAGGCGAGCATGATGATGCTGAGAGAGCAAGCACACTGGAGCTGAGACAG 300  
 DB 258 CAAGGCGAGCATGATGATGCTGAGAGAGCAAGCACACTGGAGCTGAGACAG 317  
 QY 301 GCCCAACTCTTAACGGAGGAGCAGATGGGGAAATTTTGAACATGGGCGCAACCTGATC 360  
 DB 318 GCCCAACTCTTAACGGAGGAGCAGATGGGGAAATTTTGAACATGGGCGCAACCTGATC 377  
 QY 361 CAGCAATGCGCGTGAAGTGAAGAGGCTTCGGGTTTGAAGCTCTTTCAGTGAAGA 420  
 DB 378 CAGCAATGCGCGTGAAGTGAAGAGGCTTCGGGTTTGAAGCTCTTTCAGTGAAGA 437  
 QY 421 AAAGTTACGGTAATATATCTGATCATGACGGTATCGACAGAGAGCAACCGGCTAAC 480  
 DB 438 AAAGTTACGGTAATATATCTGATCATGACGGTATCGACAGAGAGCAACCGGCTAAC 497

QY 481 TACGTCCGACAGCCGCGGTAATACGTAGGTGCAAGCGTTATCGAATTACTGAGGCGT 540  
 DB 498 TACGTCCGACAGCCGCGGTAATACGTAGGTGCAAGCGTTATCGAATTACTGAGGCGT 557  
 QY 541 AAAGGTGGCGAGCGGCTTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 600  
 DB 558 AAAGGTGGCGAGCGGCTTTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 617  
 QY 601 TCGCTTTGAACCTACAGGCTAGAGTGGCGAGGAGGAGTGAATTCATGTGTAGCAG 660  
 DB 618 TCGCTTTGAACCTACAGGCTAGAGTGGCGAGGAGGAGTGAATTCATGTGTAGCAG 677  
 QY 661 TGAATGCGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 720  
 DB 678 TGAATGCGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 737  
 QY 721 GACGCTCATGACAGAAAGCGTGGGAGCAAGAGATTAGATACCTGCTAGTCCAGCC 780  
 DB 738 GACGCTCATGACAGAAAGCGTGGGAGCAAGAGATTAGATACCTGCTAGTCCAGCC 797  
 QY 781 CTAAACGATGCTAAGTGTGTTGGGCTTTATAGGCTTGTAGCAAGCTTAACGCTGA 840  
 DB 798 CTAAACGATGCTAAGTGTGTTGGGCTTTATAGGCTTGTAGCAAGCTTAACGCTGA 857  
 QY 841 AGTTGACCGGCTGGGAGTACGCTGCAAGATTAAACCTAAAGGAATTGACGGGAGCC 900  
 DB 858 AGTTGACCGGCTGGGAGTACGCTGCAAGATTAAACCTAAAGGAATTGACGGGAGCC 917  
 QY 901 GCACAAGCGGCTGATTTATGATTAATTCATGACGCAAGCAAAACCTTACCTACCTT 960  
 DB 918 GCACAAGCGGCTGATTTATGATTAATTCATGACGCAAGCAAAACCTTACCTACCTT 977  
 QY 961 GACATGTACGAAATTTTCTAGAGTATGATGCTGCTGGGAGAGCTTAACACAGTGTCT 1019  
 DB 978 GACATGTACGAAATTTTCTAGAGTATGATGCTGCTGGGAGAGCTTAACACAGTGTCT 1037  
 QY 1020 GCATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1079  
 DB 1038 GCATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1097  
 QY 1080 CCTGTCTAATTAATGCGATCATTTTGTGGGCACTTTAATGAGACTGCCGTGACAAAC 1139  
 DB 1098 CCTGTCTAATTAATGCGATCATTTTGTGGGCACTTTAATGAGACTGCCGTGACAAAC 1157  
 QY 1140 GGAAGAGGTGGGAGTGAAGTCAATCTCTCATAGGCCCTTAATGGTGAAGGCTTCAACCTGA 1199  
 DB 1158 GGAAGAGGTGGGAGTGAAGTCAATCTCTCATAGGCCCTTAATGGTGAAGGCTTCAACCTGA 1217  
 QY 1200 ATACAATGGCGGCTACAGAGGCTTGCACACCGCGAGGGGAGCTAATCTCAGAAAGCGC 1259  
 DB 1218 ATACAATGGCGGCTACAGAGGCTTGCACACCGCGAGGGGAGCTAATCTCAGAAAGCGC 1277  
 QY 1260 GTCTAGTGCCTGATGAGTCTGCAACTGCACTCCGTGAAGTGGAAATGCTAGTAATCG 1319  
 DB 1278 GTCTAGTGCCTGATGAGTCTGCAACTGCACTCCGTGAAGTGGAAATGCTAGTAATCG 1337  
 QY 1320 CGATACGATGCTCGGCGTGAATACGTTCCGGGCTTGTACACACCGCCGCTCACACA 1379  
 DB 1338 CGATACGATGCTCGGCGTGAATACGTTCCGGGCTTGTACACACCGCCGCTCACACA 1397  
 QY 1380 TGGAGTGGGTTTCCAGAAACAGATGCTTAACCGTAAGAGGAGGCGCTTGCACAGGTG 1439  
 DB 1398 TGGAGTGGGTTTCCAGAAACAGATGCTTAACCGTAAGAGGAGGCGCTTGCACAGGTG 1457  
 QY 1440 AGATTCACTGAGGGGTG 1457  
 DB 1458 AGATTCACTGAGGGGTG 1475

RESULT 9  
 US-10-659-983A-20  
 ; Sequence 20, Application US/10659983A  
 ; Publication No. US20040157313A1

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GENERAL INFORMATION:
APPLICANT: Hovanec, Timothy A
TITLE OF INVENTION: Ammonia-Oxidizing Bacteria
FILE REFERENCE: 81289-28479
CURRENT APPLICATION NUMBER: US/10/659,983A
CURRENT FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: US 09/573,684
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: US 60/386,217
PRIOR FILING DATE: 2002-09-19
PRIOR APPLICATION NUMBER: US 60/386,218
PRIOR FILING DATE: 2002-09-19
PRIOR APPLICATION NUMBER: US 60/386,219
PRIOR FILING DATE: 2002-09-19
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn version 3.2
SEQ ID NO 20
LENGTH: 1491
TYPE: DNA
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: N. Aestuarii-like AOB Bf1c1one57.165 rDNA
US-10-659-983A-20

Query Match      95.5%; Score 1391.6; DB 7; Length 1491;
Best Local Similarity 97.6%; Pred. No. 0;
Matches 1423; Conservative 0; Mismatches 34; Indels 1; Gaps 1;

QY 1 ATTGAAGCTGGCGGCGCATGCTTTACACATGCAAGTCGAACGGGACACGAGATGCTTGAT 60
DB 18 ATTGAAGCTGGCGGCGCATGCTTTACACATGCAAGTCGAACGGGACACGAGATGCTTGAT 77
QY 61 CTGGTGCGAGTGCGCGACGAGTGATATGATCGAATCGAATCGAAGAGGCGGCTA 120
DB 78 CTGGTGCGAGTGCGCGACGAGTGATATGATCGAATCGAATCGAAGAGGCGGCTA 137
QY 121 ACGCATCGAAGATGTGCTAATACCGCATATCTCTTAAGAGAGAAAGCAGGGGATCGAAA 180
DB 138 ACGCATCGAAGATGTGCTAATACCGCATATCTCTTAAGAGAGAAAGCAGGGGATCGAAA 197
QY 181 GACCTGCGCTTTTGGAGCGGCGCATGCTGATTTAGTGTGAGGGGTTAAAGGCTTAC 240
DB 198 GACCTGCGCTTTTGGAGCGGCGCATGCTGATTTAGTGTGAGGGGTTAAAGGCTTAC 257
QY 241 CAAGCGCATGATCGATGATGCTGAGAGAGACACGCACTGCGAATGAGACAG 300
DB 258 CAAGCGCATGATCGATGATGCTGAGAGAGACACGCACTGCGAATGAGACAG 317
QY 301 GCCCAAGCTCTTACGCGAGGAGCAGATGCGGGAATTTTGGACATATGGCGCAAGCTGATC 360
DB 318 GCCCAAGCTCTTACGCGAGGAGCAGATGCGGGAATTTTGGACATATGGCGCAAGCTGATC 377
QY 361 CAGCAATGCCCCCGTGAAGAGAGAGCCCTGCGGTTTGAAGCTCTTCAAGTCGAGAGA 420
DB 378 CAGCAATGCCCCCGTGAAGAGAGAGCCCTGCGGTTTGAAGCTCTTCAAGTCGAGAGA 437
QY 421 AAAGTTACGGTAATATCTGTAATCTGATCGATGACGATGACAGAGAAGACACCGGCTAAC 480
DB 438 AAAGTTACGGTAATATCTGTAATCTGATCGATGACGATGACAGAGAAGACACCGGCTAAC 497
QY 481 TACGTCGACAGACCGCGGTAAATCTGAGGTCGAGCGTTATGGAATTAATCTGGCGCT 540
DB 498 TACGTCGACAGACCGCGGTAAATCTGAGGTCGAGCGTTATGGAATTAATCTGGCGCT 557
QY 541 AAAGGTCGCGAGCGGCTTTTGTATGACATGTAATATCCCGGCTTAACTGAGGAT 600
DB 558 AAAGGTCGCGAGCGGCTTTTGTATGACATGTAATATCCCGGCTTAACTGAGGAT 617
QY 601 TGCCTTTGAAATCTAAGAGCTGAGTGTGCGAGAGAGGAGGAAATTCATGTAGCAG 660
DB 618 TGCCTTTGAAATCTAAGAGCTGAGTGTGCGAGAGAGGAGGAAATTCATGTAGCAG 677
QY 661 TGAATGCGTAGATATGGAAGAAATCGATGCGGAAGGACGCTCTCGGGTTAACT 720

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DB 678 TGAATGCGTAGATATGGAAGAAATCGATGCGGAAGGACGCGCTCGGTTAACT 737
QY 721 GACGCTATGACAGAAAGCGTGGGAGCAAAACAGATTAGATCCTGTGATCCAGCC 780
DB 738 GACGCTATGACAGAAAGCGTGGGAGCAAAACAGATTAGATCCTGTGATCCAGCC 797
QY 781 CTAACGATGTCATCTGTTGTTGGGCTTATTAAGCTTGTGTAACGAAGCTTAAGCGCTGA 840
DB 798 CTAACGATGTCATCTGTTGTTGGGCTTATTAAGCTTGTGTAACGAAGCTTAAGCGCTGA 857
QY 841 AGTTGACCGCTGGGAGTACCGTGCAGATTTAACTCAAGAGATTGACGGGAGCC 900
DB 858 AGTTGACCGCTGGGAGTACCGTGCAGATTTAACTCAAGAGATTGACGGGAGCC 917
QY 901 GCACAGCGGTGATTAATGATTAATTCGATGCAACGCGAAAACCTTAACCTTACCCTT 960
DB 918 GCACAGCGGTGATTAATGATTAATTCGATGCAACGCGAAAACCTTAACCTTACCCTT 977
QY 961 GACATGAGCGAATTTTCTAGATTAATGATTAATTCGATGCAACGCGAAAACCTTACCCTT 1019
DB 978 GACATGAGCGAATTTTCTAGATTAATGATTAATTCGATGCAACGCGAAAACCTTACCCTT 1037
QY 1020 GCATGCGCTGTCGAGCTCGTGTGAGATGTTGGTTAAGTCCGCAACGAGCGCAAC 1079
DB 1038 GCATGCGCTGTCGAGCTCGTGTGAGATGTTGGTTAAGTCCGCAACGAGCGCAAC 1097
QY 1080 CTTGTGATTAATTCGATGATTAATGATTAATTCGATGCAACGCGAAAACCTTACCCTT 1139
DB 1098 CTTGTGATTAATTCGATGATTAATGATTAATTCGATGCAACGCGAAAACCTTACCCTT 1157
QY 1140 GAGAGAGTGGGAGTACGTCATGCTTCAATGCGCTTATGAGGCTTCAACGTA 1199
DB 1158 GAGAGAGTGGGAGTACGTCATGCTTCAATGCGCTTATGAGGCTTCAACGTA 1217
QY 1200 ATTAAGTGGCGCGTACAGAGGTTGCCAACCCCGAGGGGAGTAAATTCAGAAAGGCGC 1259
DB 1218 ATTAAGTGGCGCGTACAGAGGTTGCCAACCCCGAGGGGAGTAAATTCAGAAAGGCGC 1277
QY 1260 GTCTAGTCCGATCGAGATCTGCAATCTGCACTCCGTGAAGTGGAAATGCTAGTAATCG 1319
DB 1278 GTCTAGTCCGATCGAGATCTGCAATCTGCACTCCGTGAAGTGGAAATGCTAGTAATCG 1337
QY 1320 CGATGACATGTCGCGGTGAATACGTTCCCGGCTTGTACACACCGCCGCTACACCA 1379
DB 1338 CGATGACATGTCGCGGTGAATACGTTCCCGGCTTGTGTACACACCGCCGCTACACCA 1397
QY 1380 TGGAGTGGGTTTCAACAGAAAGCAGTACTAACCGTTAAGAGAGGCGCTTGCCAGGCTG 1439
DB 1398 TGGAGTGGGTTTCAACAGAAAGCAGTACTAACCGTTAAGAGAGGCGGCTTGCCAGGCTG 1457
QY 1440 AGATTGATGACTGGGCTG 1457
DB 1458 AGATTGATGACTGGGCTG 1475

RESULT 10
US-10-659-948A-19
Sequence 19, Application US/10659948A
Publication No. US20040101946A1
GENERAL INFORMATION:
APPLICANT: Hovanec, Timothy A
TITLE OF INVENTION: Method of Using Ammonia-Oxidizing Bacteria
FILE REFERENCE: 81289-294309
CURRENT APPLICATION NUMBER: US/10/659,948A
CURRENT FILING DATE: 2003-09-10
PRIOR APPLICATION NUMBER: US 09/573,684
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: US 60/386,217
PRIOR FILING DATE: 2002-09-19
PRIOR APPLICATION NUMBER: US 60/386,218
PRIOR FILING DATE: 2002-09-19
PRIOR APPLICATION NUMBER: US 60/386,219

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PRIOR FILING DATE: 2002-09-19  
 NUMBER OF SEQ ID NOS: 23  
 SOFTWARE: PatentIn version 3.2  
 SEQ ID NO 19  
 LENGTH: 1494  
 TYPE: DNA  
 ORGANISM: Unknown  
 FEATURE:  
 OTHER INFORMATION: N. Aestuarii-like AOB Paclone31 16S rDNA  
 US-10-659-948A-19

Query Match 93.3%; Score 1359.2; DB 7; Length 1494;  
 Best Local Similarity 96.3%; Pred. No. 0;  
 Matches 1402; Conservative 0; Mismatches 53; Indels 1; Gaps 1;

1 ATTGAACGCTGCGGCGATGCTTTACATGCAAGTCGACGCGACGCGATCTTCAT 60  
 19 ATTGAACGCTGCGGCGATGCTTTACATGCAAGTCGACGCGACGCGATCTTCAT 78  
 61 CTGCTGCGGCGATGCTGCGGCGATGCTTTACATGCAAGTCGACGCGATCTTCAT 120  
 79 CTGCTGCGGCGATGCTGCGGCGATGCTTTACATGCAAGTCGACGCGATCTTCAT 138  
 121 ACGCATCGAAGAGTGTCTAATACCGCATATCTTAAGGAGGAAAGCGGAGTGA 180  
 139 ACGCATCGAAGAGTGTCTAATACCGCATATCTTAAGGAGGAAAGCGGAGTGA 198  
 181 GACCTTGCGCTTTGAGCGCGCGATGCTGATTAGTGTGCGGAGTGAAGGCTTAC 240  
 199 GACCTTGCGCTTTGAGCGCGCGATGCTGATTAGTGTGCGGAGTGAAGGCTTAC 258  
 241 CAAGGCGAGTCAATGATGCTGCTGAGAGGAGCAAGCAAGTCTGAGTCAAGTCA 300  
 259 CAAGGCGAGTCAATGATGCTGCTGAGAGGAGCAAGCAAGTCTGAGTCAAGTCA 318  
 301 GCCCAGACTCTTACGCGGAGGAGCAGATGCGGAGTGAAGTGAAGTGAAGTGA 360  
 319 GCCCAGACTCTTACGCGGAGGAGCAGATGCGGAGTGAAGTGAAGTGAAGTGA 378  
 361 CAGCAATGCGCGCTGAGTGAAGAGGCTTGGGCTTGAAGTCTTTCAGTGAAGA 420  
 379 CAGCAATGCGCGCTGAGTGAAGAGGCTTGGGCTTGAAGTCTTTCAGTGAAGA 438  
 421 AAGGTTAGGTTAATATGATGATCATGATCGATCGAAGAGGAGTCAAGGCTTAC 480  
 439 AAGGTTAGGTTAATATGATGATCATGATCGATCGAAGAGGAGTCAAGGCTTAC 498  
 481 TACGTCACGACGCGCGGTTAATACGTTAGGAGTCAAGGCTTAACTGAGGCGT 540  
 499 TACGTCACGACGCGCGGTTAATACGTTAGGAGTCAAGGCTTAACTGAGGCGT 558  
 541 AAGGTTAGGTTAATATGATGATCATGATCGATCGAAGAGTCAAGGCTTAACT 600  
 559 AAGGTTAGGTTAATATGATGATCATGATCGATCGAAGAGTCAAGGCTTAACT 618  
 601 TGGCTTTGAATCTCAAGGTTAAGTGTGCGCAAGGAGTGAATTTCCATGTGACAG 660  
 619 TGGCTTTGAATCTCAAGGTTAAGTGTGCGCAAGGAGTGAATTTCCATGTGACAG 678  
 661 TGAATGCTAGAGTATGGAAGATCATGATGCGCAAGGAGTGAATTTCCATGTGAC 720  
 679 TGAATGCTAGAGTATGGAAGATCATGATGCGCAAGGAGTGAATTTCCATGTGAC 738  
 721 GACGCTCATGACGAAGCGTGGGAGCAAAACGATTAGATCCTGTGATGACGCC 780  
 739 GACGCTCATGACGAAGCGTGGGAGCAAAACGATTAGATCCTGTGATGACGCC 798  
 781 CTAAAGAGTCACTAGTGTGTTGGGCTTATAGGCTTGTGTAAGGAGTCAAGGCT 840  
 799 CTAAAGAGTCACTAGTGTGTTGGGCTTATAGGCTTGTGTAAGGAGTCAAGGCT 858  
 841 AGTTGACCGGCTGGGAGTACGCTCCAGATTAACTCAAGGATTGACCGGAGGCC 900

859 AGTTGACCGGCTGGGAGTACGCTCCAGATTAACTCAAGGATTGACGGGAGGCC 918  
 901 GACCAAGCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 960  
 919 GACCAAGCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 978  
 961 GACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1019  
 979 GACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1038  
 1020 GCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1079  
 1039 GCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1098  
 1080 CTTGTCATTAATGTCATTAATGTCATTAATGTCATTAATGTCATTAATGTCAT 1139  
 1099 CTTGTCATTAATGTCATTAATGTCATTAATGTCATTAATGTCATTAATGTCAT 1158  
 1140 GAGGAGAGTGGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1199  
 1159 GAGGAGAGTGGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 1218  
 1200 ATACAATGCGCGCTACAGAGGCTTCCAAACCGGAGGAGGAGTGAATCTCAG 1259  
 1219 ATACAATGCGCGCTACAGAGGCTTCCAAACCGGAGGAGGAGTGAATCTCAG 1278  
 1260 GTGCTAGTCCGATGCGATGCGATGCGATGCGATGCGATGCGATGCGATGCG 1319  
 1279 GTGCTAGTCCGATGCGATGCGATGCGATGCGATGCGATGCGATGCGATGCG 1338  
 1320 CGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1379  
 1339 CGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1398  
 1380 TGGAGTGGGTTTCAACCAAGCAGATGATGATGATGATGATGATGATGATGAT 1439  
 1399 TGGAGTGGGTTTCAACCAAGCAGATGATGATGATGATGATGATGATGATGAT 1458  
 1440 AGATTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1455  
 1459 TGGTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1474

RESULT 11  
 US-10-659-980A-19  
 ; Sequence 19, Application US/10659980A  
 ; Publication No. US20040106133A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hovaneq, Timothy A  
 ; TITLE OF INVENTION: Method for Detecting Ammonia-Oxidizing Bacteria  
 ; FILE REFERENCE: 81289-284781  
 ; CURRENT APPLICATION NUMBER: US/10/659,980A  
 ; PRIOR FILING DATE: 2003-09-10  
 ; PRIOR APPLICATION NUMBER: US 09/573,684  
 ; PRIOR FILING DATE: 2000-05-19  
 ; PRIOR APPLICATION NUMBER: US 60/386,217  
 ; PRIOR FILING DATE: 2002-09-19  
 ; PRIOR APPLICATION NUMBER: US 60/386,218  
 ; PRIOR FILING DATE: 2002-09-19  
 ; PRIOR APPLICATION NUMBER: US 60/386,219  
 ; PRIOR FILING DATE: 2002-09-19  
 ; NUMBER OF SEQ ID NOS: 23  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 19  
 ; LENGTH: 1494  
 ; TYPE: DNA  
 ; ORGANISM: Unknown  
 ; FEATURE:  
 ; OTHER INFORMATION: N. Aestuarii-like AOB Paclone31 16S rDNA  
 US-10-659-980A-19

Query Match 93.3%; Score 1359.2; DB 7; Length 1494;  
 Best Local Similarity 96.3%; Pred. No. 0;



| Matches 1402; Conservative 0; Mismatches 53; Indels 1; Gaps 1; |      |   |      |
|--|------|---|------|
| Qy   | 1    | ATTGAAACGCTGCGCGCATGCTTTTACATGCAAGTCGAACGGCAGCACGGATGCTTGAT | 60   |
| Db   | 19   | ATTGAAGCTGGCGCATGCTTTTACATGCAAGTCGAACGGCAGCACGGGCTTGAC      | 78   |
| Qy   | 61   | CTGTGGGAGTGGCGGACGGGTGATATGATGCGAACGTCATCAAGAGGGGGGTA       | 120  |
| Db   | 79   | CTGTGGGAGTGGCGGACGGGTGATATGATGCGAACGTCATCAAGAGGGGGGTA       | 138  |
| Qy   | 121  | ACGATCGAAGATGTGTAATACCGCATATATCTGAAGAGAGAGAGCGGGATCGAA      | 180  |
| Db   | 139  | ACGATCGAAGATGTGTAATACCGCATATATCTGAAGAGAGAGAGCGGGATCGAA      | 198  |
| Qy   | 181  | GACCTTGGCTTTTGGACGGCGCATGCTGATTAAGTGTGGGTAAAGGCTTAC         | 240  |
| Db   | 199  | GACCTTGGCTTTTGGACGGCGCATGCTGATTAAGTGTGGGTAAAGGCTTAC         | 258  |
| Qy   | 241  | CAAGCGCATCATGATGTTGTTGAGAGAGACGACCGCCACTGGGACTGAGACACG      | 300  |
| Db   | 259  | CAAGCGCATCATGATGTTGTTGAGAGAGACGACCGCCACTGGGACTGAGACACG      | 318  |
| Qy   | 301  | GCCGACCTCTTACCGGAGGCGAGAGTGGGGAATTTTGGACAATGGCGCAAGCTTATC   | 360  |
| Db   | 319  | GCCGACCTCTTACCGGAGGCGAGAGTGGGGAATTTTGGACAATGGCGCAAGCTTATC   | 378  |
| Qy   | 361  | CAGCAATCCCGGTGAGTGAAGAGGCTTCGGGTTGTAAGCTCTTTCAGTCGAGAA      | 420  |
| Db   | 379  | CAGCAATCCCGGTGAGTGAAGAGGCTTCGGGTTGTAAGCTCTTTCAGTCGAGAA      | 438  |
| Qy   | 421  | AAAGGTACGTAATTAATCGTACTCATGACGCTATGCAAGAGAGAGAGAGCGGCTAC    | 480  |
| Db   | 439  | AAAGGTGTGCTAATTAATCACTTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAG       | 498  |
| Qy   | 481  | TACGTCAGACGACCGCGGTATATGTAAGGTCGACGCTTATCGAATTTCTGGGCT      | 540  |
| Db   | 499  | TACGTCAGACGACCGCGGTATATGTAAGGTCGACGCTTATCGAATTTCTGGGCT      | 558  |
| Qy   | 541  | AAAGGTGCGGACGGGCTTTTGAATGTCAGATGTGAATCCCGGGCTTTTACCTGGGAT   | 600  |
| Db   | 559  | AAAGGTGCGGACGGGCTTTTGAATGTCAGATGTGAATCCCGGGCTTTTACCTGGGAT   | 618  |
| Qy   | 601  | TGCGTTGAACTAACAAGCTGATGTGGCGAGAGGAGTGGAAATTCATGTGAGCAG      | 660  |
| Db   | 619  | TGCGTTGAACTAACAAGCTGATGTGGCGAGAGGAGTGGAAATTCATGTGAGCAG      | 678  |
| Qy   | 661  | TGAATGTGTAAGATATGAGAGAAATCATGATGGGAGAGAGAGAGAGAGAGAGAG      | 720  |
| Db   | 679  | TGAATGTGTAAGATATGAGAGAAATCATGATGGGAGAGAGAGAGAGAGAGAGAG      | 738  |
| Qy   | 721  | GACGCTCATGACGAAGGCGTGGGAGCAAAACAGATTAAGATACCTGTGTGACAGCC    | 780  |
| Db   | 739  | GACGCTCATGACGAAGGCGTGGGAGCAAAACAGATTAAGATACCTGTGTGACAGCC    | 798  |
| Qy   | 781  | CTAAACGATGTCACTAGTTGTTGGCCCTTATTAAGCTTGGTGAAGAGCTAACCGCTGA  | 840  |
| Db   | 799  | CTAAACGATGTCACTAGTTGTTGGCCCTTATTAAGCTTGGTGAAGAGCTAACCGCTGA  | 858  |
| Qy   | 841  | AGTTGACCGCTGGGAGATGACGCTGCAAGATTTAAACCTCAAGAGATTTGACGGGAGCC | 900  |
| Db   | 859  | AGTTGACCGCTGGGAGATGACGCTGCAAGATTTAAACCTCAAGAGATTTGACGGGAGCC | 918  |
| Qy   | 901  | GCACAGCGGTGATATATGATTAATTCAGTGAACGCGAAGAAACCTTACCTTACCTT    | 960  |
| Db   | 919  | GCACAGCGGTGATATATGATTAATTCAGTGAACGCGAAGAAACCTTACCTTACCTT    | 978  |
| Qy   | 961  | GACATGTAGCAAAATTTTCAAGATAGATTAAGT-CTTCGGGAGAGCTTAACAAGTGT   | 1019 |
| Db   | 979  | GACATGTAGCAAAATTTTCAAGATAGATTAAGT-CTTCGGGAGAGCTTAACAAGTGT   | 1038 |
| Qy   | 1020 | GCATGGCTGTGCTAGCTGTGTCGATGATGTTGGGTTAAGTCCCGCAACAGAGCGAAC   | 1079 |
| Db   | 1039 | GCATGGCTGTGCTAGCTGTGTCGATGATGTTGGGTTAAGTCCCGCAACAGAGCGAAC   | 1098 |

|    |      |  |      |
|----|------|--|------|
| Qy | 1080 | CCTTGTCAATTAATTCGCAATCATTTGTTGGGCACTTTAATGAGACTGGCGGAGCAAAAC | 1139 |
| Db | 1099 | CCTTGTCAATTAATTCGCAATCATTTGTTGGGCACTTTAATGAGACTGGCGGAGCAAAAC | 1158 |
| Qy | 1140 | GGAGGAAGTGGGATGACGTCAGATGCTTATGAGGCTTATGAGGCTTCAACGTA        | 1199 |
| Db | 1159 | GGAGGAAGTGGGATGACGTCAGATGCTTATGAGGCTTATGAGGCTTCAACGTA        | 1218 |
| Qy | 1200 | ATACATGCGCGTACAGAGGTTGCCAACCCGCGAGGGGAGCTTAATCTGAAGAGGCG     | 1259 |
| Db | 1219 | ATACATGCGCGTACAGAGGTTGCCAACCCGCGAGGGGAGCTTAATCTGAAGAGGCG     | 1278 |
| Qy | 1260 | GTCGTAGCCGGATTCGAGTGTGCAATCCGATCCGCGAATCCGGAATCCGTAATATG     | 1319 |
| Db | 1279 | GTCGTAGCCGGATTCGAGTGTGCAATCCGATCCGCGAATCCGGAATCCGTAATATG     | 1338 |
| Qy | 1320 | CGATACAGCATGTGCGGCTGAATACGTTCCGGGCTTGTACACACCGCCGTCACCA      | 1379 |
| Db | 1339 | CGATACAGCATGTGCGGCTGAATACGTTCCGGGCTTGTACACACCGCCGTCACCA      | 1398 |
| Qy | 1380 | TGGAGTGGGTTTACCAAGAGCAGTATCTAACCGTAGAGAGGCGCTTGCCAGGTG       | 1439 |
| Db | 1399 | TGGAGTGGGTTTACCAAGAGCAGTATCTAACCGTAGAGAGGCGCTTGCCAGGTG       | 1458 |
| Qy | 1440 | AGATTCATGACTGGGG   | 1455 |
| Db | 1459 | TGTCATGACTGGGG   | 1474 |

## RESULT 12

US-10-659-983A-19

Sequence 19, Application US/10659983A

Publication No. US20040157313A1

GENERAL INFORMATION:

APPLICANT: Hovaneq, Timothy A

TITLE OF INVENTION: Ammonia-Oxidizing Bacteria

FILE REFERENCE: 81289-28479

CURRENT FILING DATE: US/10/659, 983A

PRIOR APPLICATION NUMBER: US 09/573, 684

PRIOR FILING DATE: 2000-05-19

PRIOR APPLICATION NUMBER: US 60/386, 217

PRIOR FILING DATE: 2002-09-19

PRIOR APPLICATION NUMBER: US 60/386, 218

PRIOR FILING DATE: 2002-09-19

PRIOR APPLICATION NUMBER: US 60/386, 219

PRIOR FILING DATE: 2002-09-19

NUMBER OF SEQ ID NOS: 23

SOFTWARE: Patentin Version 3.2

SEQ ID NO 19

LENGTH: 1494

TYPE: DNA

ORGANISM: Unknown

FEATURE:

OTHER INFORMATION: N. Aestuarii-like AOB Paclome31 16S rDNA

US-10-659-983A-19

Query Match 93.3%; Score 1359.2; DB 7; Length 1494;  
 Best Local Similarity 96.3%; Pred. No. 0;  
 Matches 1402; Conservative 0; Mismatches 53; Indels 1; Gaps 1;

|    |     |  |     |
|----|-----|--|-----|
| Qy | 1   | ATTGAACGCTGCGCGCATGCTTTTACATGCAAGTCGAACGGCAGCACGGATGCTTGAT | 60  |
| Db | 19  | ATTGAAGCTGGCGCATGCTTTTACATGCAAGTCGAACGGCAGCACGGGCTTGAC     | 78  |
| Qy | 61  | CTGTGGGAGTGGCGGACGGGTGATATGATGCGAACGTCATCAAGAGGGGGGTA      | 120 |
| Db | 79  | CTGTGGGAGTGGCGGACGGGTGATATGATGCGAACGTCATCAAGAGGGGGGTA      | 138 |
| Qy | 121 | ACGATCGAAGATGTGTAATACCGCATATATCTGAAGAGAGAGAGCGGGATCGAA     | 180 |
| Db | 139 | ACGATCGAAGATGTGTAATACCGCATATATCTGAAGAGAGAGAGCGGGATCGAA     | 198 |





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Db      555 AAGGGGCGCGAGCGCTTTGTAGTCAAGTGTGAATCCCGGGCTTAACTGGGAT 614
Qy      601 TGCCTTTGAAACTCAAGAGCTAGAGTGTGCGAGAGAGTGAATTCATGTGTAGAG 660
Db      615 TGCCTTTGAAACTCAAGAGCTAGAGTGTGCGAGAGAGTGAATTCATGTGTAGAG 674
Qy      661 TGAATTCGTAGAGATATGGAAGAACTCGATGCGGAAGGAGCCTCTGGGTTAACT 720
Db      675 TGAATTCGTAGAGATATGGAAGAACTCGATGCGGAAGGAGCCTCTGGGTTAACT 734
Qy      721 GAGGCTATGACGAAGAGCGGGGAGGAACAGAGATTAGATCCCTGTGTGTACAGCC 780
Db      735 GAGGCTATGACGAAGAGCGGGGAGGAACAGAGATTAGATCCCTGTGTGTACAGCC 794
Qy      781 CTAAACGATGTCAACTAGTGTGGGCTTTATTAAGCTGTGTAACGAAGCTAACGCGTGA 840
Db      795 CTAAACGATGTCAACTAGTGTGGGCTTTATTAAGCTGTGTAACGAAGCTAACGCGTGA 854
Qy      841 AGTTGACCGCTGGGAGTACGCTGCGCAAGTTAAACTCAAGGAATTGACGGGAGCC 900
Db      855 AGTTGACCGCTGGGAGTACGCTGCGCAAGTTAAACTCAAGGAATTGACGGGAGCC 914
Qy      901 GCAACAGCGGTGATTAATGTGATTAATTCGATGCAACGCGAAACCTTACCTACCTT 960
Db      915 GCAACAGCGGTGATTAATGTGATTAATTCGATGCAACGCGAAACCTTACCTACCTT 974
Qy      961 GACATGTAGCGAATTTTCTAGAGATAGATTAGTGC-TTCGGGAAACGCTAACACAGTGTCT 1019
Db      975 GACATGTAGCGAATTTTCTAGAGATAGATTAGTGC-TTCGGGAAACGCTAACACAGTGTCT 1034
Qy      1020 GCATGCGCTGTCTCACTCGTGTGTGAGATGTTGGGTTAAGTCCCGCAACGACCGCAAC 1079
Db      1035 GCATGCGCTGTCTCACTCGTGTGTGAGATGTTGGGTTAAGTCCCGCAACGACCGCAAC 1094
Qy      1080 CTTGTCAATTAATGCCATCATTTGTTGGGCACTTTAATGAGACTGCGCGGTGACAAAC 1139
Db      1095 CTTGTCAATTAATGCCATCATTTGTTGGGCACTTTAATGAGACTGCGCGGTGACAAAC 1154
Qy      1140 GAGAGAGTGGGGATGACGTCAGTCTCTCAATGCGCCCTTATGGGTAGGGCTTCAACGTA 1199
Db      1155 GAGAGAGTGGGGATGACGTCAGTCTCTCAATGCGCCCTTATGGGTAGGGCTTCAACGTA 1214
Qy      1200 ATACAAATGGGCGCTGACAGAGGTTGCGCAACCCGAGGGGAGGCTAATCTAGAAAGGCC 1259
Db      1215 ATACAAATGGGCGCTGACAGAGGTTGCGCAACCCGAGGGGAGGCTAATCTAGAAAGGCC 1274
Qy      1260 GTGCTAGTCCGGATCGGAGTGTGCAACTCGACTCGTGAAGTGGGAATCGCTAGTAATCG 1319
Db      1275 GTGCTAGTCCGGATCGGAGTGTGCAACTCGACTCGTGAAGTGGGAATCGCTAGTAATCG 1334
Qy      1320 CGGATCGAGATGTGCGCGGTGAATCGTTCCGGGCTTTGTATCACACGCGCCGCTACACA 1379
Db      1335 CGGATCGAGATGTGCGCGGTGAATCGTTCCGGGCTTTGTATCACACGCGCCGCTACACA 1394
Qy      1380 TGGGAGTGGGTTTACCAAGAGCGTATGTTAAACCTTAAGAGAGGGGCTTGCACGCGTG 1439
Db      1395 TGGGAGTGGGTTTACCAAGAGCGTATGTTAAACCTTAAGAGAGGGGCTTGCACGCGTG 1453
Qy      1440 AGATTGATGACTGG 1453
Db      1454 AGATTGATGACTGG 1467

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## RESULT 15

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; Sequence 18: Application US/10659983A
; Publication No. US20040157313A1
; GENERAL INFORMATION:
; APPLICANT: Hovaneec, Timothy A
; TITLE OF INVENTION: Ammonia-Oxidizing Bacteria
; FILE REFERENCE: 81289-28479
; CURRENT APPLICATION NUMBER: US/10/659, 983A

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; CURRENT FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: US 09/573,684
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 60/386,217
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,218
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/386,219
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 1467
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: N. Aestuarii-like AOB P4clone42 16S rDNA
US-10-659-983A-18

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Query Match      93.3%; Score 1358.8; DB 7; Length 1467;
Best Local Similarity 97.2%; Pred. No. 0;
Matches 1414; Conservative 0; Mismatches 37; Indels 3; Gaps 3;

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Qy      1  ATTGAACGCTGGGCGATGCTTTACATGCAAGTGCAGAGCGAGCAGCGATGCTTCAT 60
Db      16  ATTGAACGCTGGGCGATGCTTTACATGCAAGTGCAGAGCGAGCAGCGATGCTTCAT 75
Qy      61  CTGTGGCGAGTGGCGGACCGGTGAGTAATGCAATCGGAACGTAATCCAGAAAGGGGGTA 120
Db      76  CTGTGGCGAGTGGCGGACCGGTGAGTAATGCAATCGGAACGTAATCCAGAAAGGGGGTA 135
Qy      121  ACCGATCGAAAGATGTGCTAATCCGATATATCTTAAGAGGAAAGAGGGGATGGA 180
Db      136  ACCGATCGAAAGATGTGCTAATCCGATATATCTTAAGAGGAAAGAGGGGATGGA 195
Qy      181  GACCTTGCGCTTTGGAGCGCGGATGTCTGATTAGTATGTTGGTGGGTTAAAGCCTTAC 240
Db      196  GACCTTGCGCTTTGGAGCGCGGATGTCTGATTAGTATGTTGGTGGGTTAAAGCCTTAC 255
Qy      241  CAAGGCGAGCATGATGTTGTCTGAGAGAGACCAACGACACATGCGGACTGAGACAG 300
Db      256  CAAGGCGAGCATGATGTTGTCTGAGAGAGACCAACGACACATGCGGACTGAGACAG 315
Qy      301  GCCCAAGCTCTTACGGGAGGACGACATGGGGAATTTTGAACATATGGGCGGACCTGATC 360
Db      316  GCCCAAGCTCTTACGGGAGGACGACATGGGGAATTTTGAACATATGGGCGGACCTGATC 375
Qy      361  CAGCAATGCCGCGTGAAGTGAAGAGGCTTGGGTTGTAAGCTCTTTCAGTGCAGAGA 420
Db      376  CAGCAATGCCGCGTGAAGTGAAGAGGCTTGGGTTGTAAGCTCTTTCAGTGCAGAGA 434
Qy      421  AAGGTTAGCGTAATATCTGTGACTCATGACGTAATCGACAGAGAGACACCGGCTAAC 480
Db      435  AAGGTTAGCGTAATATCTGTGACTCATGACGTAATCGACAGAGAGACACCGGCTAAC 494
Qy      481  TACGTCCAGACACCGCGGTAAATACCTAGAGGCCAAGCGTTAATCCGAATTAATCGGGCGT 540
Db      495  TACGTCCAGACACCGCGGTAAATACCTAGAGGCCAAGCGTTAATCCGAATTAATCGGGCGT 554
Qy      541  AAGGTTGCGCAGAGCGGCTTTGTAACTCAGATGTGAATCCCGGGCTTAACTCGGGAAT 600
Db      555  AAGGTTGCGCAGAGCGGCTTTGTAACTCAGATGTGAATCCCGGGCTTAACTCGGGAAT 614
Qy      601  TGCCTTTGAAACTCAAGGCTAGAGTGTGCGAGAGAGTGAATTCATGTGTAGAG 660
Db      615  TGCCTTTGAAACTCAAGGCTAGAGTGTGCGAGAGAGTGAATTCATGTGTAGAG 674
Qy      661  TGAATTCGTAGAGATATGGAAGAACTCGATGCGGAAGGAGCCTCTGGGTTAACT 720
Db      675  TGAATTCGTAGAGATATGGAAGAACTCGATGCGGAAGGAGCCTCTGGGTTAACT 734
Qy      721  GAGGCTATGACGAAGAGCGGGGAGGAACAGAGATTAGATCCCTGTGTGTACAGCC 780

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Db      735 GACGCTCATGACGAAAGCGTGGGAGCAACAGATTAGATACCCTGCTAGTCCACGCC 794
QY      781 CTAACGATGCTCACTAGTGTGGGCTTATTAGCTTGTAAGCAAGCTAACCGCTGA 840
Db      795 CTAACGATGCTCACTAGTGTGGGCTTACTAGGCTTGTAAGCTAACCGCTGA 854
QY      841 AGTTACCGCTGGGGAAGTACGTCGCAAGATTAAACTCAAGGAATTGACGGGGAACC 900
Db      855 AGTTACCGCTGGGGAAGTACGTCGCAAGATTAAACTCAAGGAATTGACGGGGAACC 914
QY      901 GCACAGCGGTGATGATTATGATTAATTCATGCAACGCGAATAAACCCTTACCTACCTT 960
Db      915 GCACAGCGGTGATGATTATGATTAATTCATGCAACGCGAATAAACCCTTACCTACCTT 974
QY      961 GACATGTAGCCGAATTTCTAAGATAGATTAGTC-TTCGGGAACGCTAACACAGTGT 1019
Db      975 GACATGTAGCCGAATTTCTAAGATAGATTAGTC-TTCGGGAACGCTAACACAGTGT 1034
QY      1020 GCATGCTGTGCTGCTAGCTCGTGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAAC 1079
Db      1035 GCATGCTGTGCTGCTAGCTCGTGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAAC 1094
QY      1080 CTTGTCTATTATTGCCATCAATTTGGTGGCACTTTAATGACTGCGCGTGACAAAC 1139
Db      1095 CTTGTCTATTATTGCCATCAATTTGGTGGCACTTTAATGACTGCGCGTGACAAAC 1154
QY      1140 GGAGGAAGTGGGGATGACGTCAATCCTCATGCGCTTATGGGTAGGGCTTCAACGTA 1199
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QY      1200 ATACAATGCGCGGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCTAATCTCAGAAAGCGC 1259
Db      1215 ATACAATGCGCGGTACAGAGGGTTGCCAACCCGCGAGGGGGAGCTAATCTCAGAAAGCGC 1274
QY      1260 GTCGTAGTCCGATCGAGTCTGCAACTGCACTCCGTGAAGTCGGAATCGCTAGTAATCG 1319
Db      1275 GTCGTAGTCCGATCGAGTCTGCAACTGCACTCCGTGAAGTCGGAATCGCTAGTAATCG 1334
QY      1320 CGGATCAGCATGTGCGGCTGAATAGTTCGCGGCTTGTACACACCGCCGCTCACACCA 1379
Db      1335 CGGATCAGCATGTGCGGCTGAATAGTTCGCGGCTTGTACACACCGCCGCTCACACCA 1394
QY      1380 TGGAGTGGGTTTCCACGAGACAGGTAGTCTAACCGTAAGGAGGGCGCTTGCCACGGTG 1439
Db      1395 TGGAGTGGGTTTCCACGAGACAGGTAGTCTAACCGTAAGGAGGGCGCTTGCCACGGTG 1453
QY      1440 AGATTCACTGCTGG 1453
Db      1454 AGATTCACTGCTGG 1467

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Search completed: April 6, 2006, 23:35:31  
 Job time : 1288 secs

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HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: *Comamonas testosteroni* ATCC No. 5874291 11996  
 US-08-642-229A-1

Query Match 77.5%; Score 1129.2; DB 2; Length 1536;  
 Best Local Similarity 87.3%; Pred. No. 0;  
 Matches 1274; Conservative 0; Mismatches 178; Indels 8; Gaps 3;

1 ATTGAACGCTGGCGGATGCTTACACATGCAAGTGAAGCGGACGATGCTTGCAT 60  
 29 ATTGAACGCTGGCGGATGCTTACACATGCAAGTGAAGCGGACGATGCTTGCAT 85  
 61 CTGTGGCGGATGCTGGCGGATGCTTACATGCAAGTGAAGCGGACGATGCTTGCAT 120  
 86 -TGCTGACGAGTGGCGGATGCTTACATGCAAGTGAAGCGGACGATGCTTGCAT 144  
 121 AGCGATCGAAGATGCTTACATGCTTACATGCAAGTGAAGCGGACGATGCTTGCAT 180  
 145 ACTACTCGAAGATGCTTACATGCTTACATGCAAGTGAAGCGGACGATGCTTGCAT 204  
 181 GACCTTGGCGGATGCTTACATGCTTACATGCAAGTGAAGCGGACGATGCTTGCAT 240  
 205 GCGCTTGGCGGATGCTTACATGCTTACATGCAAGTGAAGCGGACGATGCTTGCAT 264  
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 601 TCGGTTAACTTACATGCTTACATGCTTACATGCAAGTGAAGCGGACGATGCTTGCAT 660  
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 685 TGAATGCGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 744  
 721 GACGCTCATGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 780  
 745 GACGCTCATGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 804  
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 805 CTAAACGATGCTTACATGCTTACATGCTTACATGCAAGTGAAGCGGATGCTTGCAT 864  
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 865 AGTTGACGCTTGGCGGATGCTTACATGCTTACATGCAAGTGAAGCGGATGCTTGCAT 924  
 901 GCAACGCGGATGCTTACATGCTTACATGCTTACATGCAAGTGAAGCGGATGCTTGCAT 960  
 925 GCAACGCGGATGCTTACATGCTTACATGCTTACATGCAAGTGAAGCGGATGCTTGCAT 984

961 GACATGACCGAATTTTCTAGAGATGATGCTCTTGGGAGCGCTAACAGAGG 1017  
 985 GACATGACCGAATTTTCTAGAGATGATGCTCTTGGGAGCGCTAACAGAGG 1044  
 1018 CTGATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1077  
 1045 CTGATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1104  
 1078 ACCCTTGTATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1137  
 1105 ACCCTTGTATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1163  
 1138 CCGAGAGAGTGGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1197  
 1164 CCGAGAGAGTGGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1223  
 1198 TAATCAATGCGGCTTACAGAGGCTTGGCCAACTGCGAGAGGAGCTTAATCTCAGAAAGC 1257  
 1224 TCATCAATGCGGCTTACAGAGGCTTGGCCAACTGCGAGAGGAGCTTAATCTCAGAAAGC 1283  
 1258 GCGTGTAGTCCGATGCGAGTCTGCAACTGCGACTGCGTGAAGTGGAAATGCTAGTAAT 1317  
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 1318 CCGGATCAGCATGCTGCGGATGAATAGCTTCCCGGCTCTTGAACACCGCCGCTCAGAC 1377  
 1344 CCGGATCAGCATGCTGCGGATGAATAGCTTCCCGGCTCTTGAACACCGCCGCTCAGAC 1403  
 1378 CATGGAGTGGGTTTACAGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1437  
 1404 CATGGAGTGGGTTTACAGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1463  
 1438 TGAGATCATGCTGCGGCTG 1457  
 1464 CCGGCTTCTGCTGCTGCGGCTG 1483

RESULT 2  
 US-09-726-774-5  
 ; Sequence 5, Application US/09726774  
 ; Patent No. 6677153  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Iversen, Patrick L.  
 ; TITLE OF INVENTION: Antisense Antibacterial Method and  
 ; FILE REFERENCE: 0450-0032.30  
 ; CURRENT APPLICATION NUMBER: US/09/726,774  
 ; PRIOR FILING DATE: 2000-11-29  
 ; PRIOR APPLICATION NUMBER: US 60/168,150  
 ; NUMBER OF SEQ ID NOS: 139  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 5  
 ; LENGTH: 1544  
 ; TYPE: DNA  
 ; ORGANISM: *Neisseria gonorrhoea*  
 US-09-726-774-5

Query Match 76.9%; Score 1119.8; DB 3; Length 1544;  
 Best Local Similarity 87.1%; Pred. No. 0;  
 Matches 1275; Conservative 0; Mismatches 182; Indels 6; Gaps 4;

1 ATTGAACGCTGGCGGATGCTTACACATGCAAGTGAAGCGGACGATGCTTGCAT 58  
 29 ATTGAACGCTGGCGGATGCTTACACATGCAAGTGAAGCGGACGATGCTTGCAT 88  
 59 ATCT--GGTGGGAGTGGCGGCGGATGCTTACACATGCAAGTGAAGCGGACGATGCTTGCAT 116  
 89 TTCTGGGAGTGGCGGCGGATGCTTACACATGCAAGTGAAGCGGACGATGCTTGCAT 148  
 117 GGTAAAGATGCAAGTGGCTTACACATGCAAGTGAAGCGGACGATGCTTGCAT 176

Db 149 GATACTGATGGAAGATCAGCTATACCGCATACGCTTGTGAGAGGAAAGCAGGAGC 208  
 Qy 177 GAAAGACCTTGCGCTTTTGGAGCGGCCCATGCTGATTAGCTAGTTGGTGGGTAAAGCC 236  
 Db 209 TTCGGGCTTTCGCTATCCGAGCGGCCGATATCTGATTAGCTGCTGGCGGGTAAAGCC 268  
 Qy 237 CTACCAAGGCGACGATCAGTGTGTTGCTGAGAGGACGACCAAGCCACACTGGGAGTGA 296  
 Db 269 CCACCAAGGCGACGATCAGTGTGTTGCTGAGAGGATGATCCGACACTGGGAGTGA 328  
 Qy 297 CACGCGCCGACCTCTACGCGGAGCGAGCGAGGAGATTTTGGACATGGGCGCAAGCCT 356  
 Db 329 CACGCGCCGACCTCTACGCGGAGCGAGCGAGGAGATTTTGGACATGGGCGCAAGCCT 388  
 Qy 357 GATCCAGCATGCGCGCTGAGTGAAGAGCCCTTGGGTTGTAAGCTCTTCACTGAG 416  
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 Db 449 AAGAAAGGCTTGTCCATATCGCGCGCGAGTGCAGTGAAGATTAAGCAGCGGC 508  
 Qy 477 TAACTACGTCGACGAGCGCGGTAAATAGTGGTGAAGCGTTAATCGGATTAATCTG 536  
 Db 509 TAACTACGTCGACGAGCGCGGTAAATAGTGGTGAAGCGTTAATCGGATTAATCTG 568  
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 Qy 657 GCAGTGAATGCTGATGATTAAGAAAGCATGATGCGAGCGAGCGCTCTGGGTAA 716  
 Db 689 GCAGTGAATGCTGATGATTAAGAAAGCATGATGCGAGCGAGCGCTCTGGGTAA 748  
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 Db 1049 GTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1108  
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 Qy 1195 ACGTAAATCAATGCGCTGACAGAGGTTGCCAAGCGGCGAGGAGGAGGAGGAGGAGGAG 1254  
 Db 1229 ACGTAAATCAATGCGCTGACAGAGGTTGCCAAGCGGCGAGGAGGAGGAGGAGGAGGAG 1288

Qy 1255 AGCGGCTGCTGATGCTGCGAGTGTGCACTGACTCCGCTGAGAGTGGAAATGCTAGT 1314  
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 Qy 1315 AATCGGATGCTGATGCTGCGAGTGTGCACTGACTCCGCTGAGAGTGGAAATGCTAGT 1374  
 Db 1349 AATCGGATGCTGATGCTGCGAGTGTGCACTGACTCCGCTGAGAGTGGAAATGCTAGT 1408  
 Qy 1375 CACCATGAGTGGGATTTCAACAGAGCAGATGCTTAACTGAGAGGAGGAGGAGGAGGAG 1434  
 Db 1409 CACCATGAGTGGGATTTCAACAGAGCAGATGCTTAACTGAGAGGAGGAGGAGGAGGAG 1468  
 Qy 1435 CGGTGATGCTGATGCTGCGAGTGTGCACTGACTCCGCTGAGAGTGGAAATGCTAGT 1491  
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 RESULT 3  
 US-08-114-695A-7  
 ; Sequence 7, Application US/08114695A  
 ; Patent No. 5508193  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Mandelbaum, Raphael T.  
 ; APPLICANT: Mackett, Lawrence P.  
 ; TITLE OF INVENTION: DEGRADATION OF S-TRIAZINES IN SOIL AND  
 ; NUMBER OF SEQUENCES: 8  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: SCHEGMAN, LUNDBERG & WOESSNER, P.A.  
 ; STREET: 3500 IDS CENTER  
 ; CITY: MINNEAPOLIS  
 ; STATE: MN  
 ; COUNTRY: USA  
 ; ZIP: 55402  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/114,695A  
 ; FILING DATE: 31-Aug-1993  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: MUSTING, ANN M.  
 ; REGISTRATION NUMBER: 33,977  
 ; REFERENCE/DOCKET NUMBER: 600.268US1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 612-339-0331  
 ; TELEFAX: 612-339-3061  
 ; INFORMATION FOR SEQ ID NO: 7:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1536 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: rRNA  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: Pseudomonas testosteroni  
 ; US-08-114-695A-7  
 Query Match 76.7%; Score 1118.2; DB 2; Length 1536;  
 Best Local Similarity 70.0%; Pred. No. 0;  
 Matches 1022; Conservative 252; Mismatches 178; Indels 9; Gaps 4;  
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 Db 28 AATGAAGCTGCGGAGT-GCTTACATGCAAGTCAACGCGACACGAGTGTGCA 84  
 Qy 60 TCTGTGCGAGTGGCGGAGTGGTGAATGATGATGCAAGTGTGCAAGAGGAGGAGT 119  
 Db 85 -AUGCUGACGAGUGGCGAAGCGGUGAGUUAUACAUCCGAAACUGCCUAGUGAGGAGAU 143

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QY 120 AAGCATCGAAGATGTCTAATACCGCATATCTTAAGAGAGAAAGAGAGATGAA 179
DB 144 AACUACUCAAAGAGUAGUUAUCCGCAUAGUUAUACGAAUGAAAGCAGGGGACUUC 203
QY 180 AGACCTTGCCCTTTTGAAGGGCCGATGTCTGATTACTGATTGTTGGTTAAAGGCTA 239
DB 204 GGGCCUUGUCUUAAGAGCGGCUAGAGGAGAUUAGUAGUUGUGGGUAAAGGCUUA 263
QY 240 CCAAGGCGAATCATGATGTTGCTGTGAGAGACGACACGACACCTGAGAGCTGAGAC 269
DB 264 CCAAGCCUGGAGUUCUAGUCUAGUAGAGAGACGACGACACGAGAGAGAGAGAC 323
QY 300 GGGCCAGACTCTTAAGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 359
DB 324 GGGCCAGACTCTTAAGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 383
QY 360 CCAAGCATGCGGCTGTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 419
DB 384 CCAAGCATGCGGCTGTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 443
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DB 444 AAAAGCTUGGGGCUAUAUCCCGGGUUAUCCGUAUCCGUAUAUAGCAACCGGCUA 503
QY 480 CTACGTGCGAGCAGCCGCGGTAATATGAGAGAGAGAGAGAGAGAGAGAGAGAG 539
DB 504 CUAAGUCCAGAGCAGCCGCGUUAUACGUAAGUCCAGAGAGAGAGAGAGAGAGAG 563
QY 540 TAAAGGTGGGAGCGGCTTTGTAATCAGATGTGAATCCCGGGCTTAAGCTGGAA 599
DB 564 UAAAGCGUGGCGAGCGGCUUUAUAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 623
QY 600 TTGCGTTGAACTAAGAGCTAGATGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 659
DB 624 CUGGCAUUGUAGACUAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 683
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DB 684 GTGAATGCGTAGATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 743
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DB 924 CGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 983
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QY 1077 AACCTGTGATTAATTTGATGCTGTTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1136
DB 1104 AACCTGTGATTAATTTGATGCTGTTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1162
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QY 1197 GTAATCAATGCGCGCTACAGAGGTTGCCAACCCCGAGGGGAGAGATGTCAGAAAG 1256
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DB 1283 CCAAGUAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1342
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DB 1343 UCGUAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1402
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QY 1437 GTGAGATGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1463
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RESULT 4
US-09-342-579-1
; Sequence 1, Application US/09342579
; Patent No. 6187569
; GENERAL INFORMATION:
; APPLICANT: BRAMUCCI, MICHAEL G.
; APPLICANT: MCCURTEN, CAROL M.
; APPLICANT: NAGARAJAN, VASANTHA
; APPLICANT: THOMAS, STUART M.
; TITLE OF INVENTION: Microbial Production of Terephthalic Acid and
; TITLE OF INVENTION: Isophthalic Acid
; FILE REFERENCE: CL-1257
; CURRENT APPLICATION NUMBER: US/09/342,579
; EARLIER FILING DATE: 1999-06-29
; EARLIER APPLICATION NUMBER: 60/091,645
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 1
; LENGTH: 1451
; TYPE: DNA
; ORGANISM: Burkholderia sp.
US-09-342-579-1

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Query Match 76.0%; Score 1108; DB 3; Length 1451;
Best Local Similarity 87.2%; Pred. No. 0;
Matches 1252; Conservative 0; Mismatches 175; Indels 9; Gaps 3;

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QY 71 GTGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 130
DB 71 GTGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 130
QY 131 AGATGTCTAATACCGCATATATCTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 190
DB 131 AGCGGATTAATACCGCATATATCTTAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 190
QY 191 TTTTGGAGGCGGCGATGTCTGATTAGCTAGTGTGGGTAAAGGCTTACCAAGGAGAG 250
DB 191 TACAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 250
QY 251 ATCAGATGTTGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 310
DB 251 ATCTGTACTGTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 310
QY 311 CTACGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 370
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QY 371 GCGTGTGTAAGAGAGCCCTTCGGGTTGTAAGCTCTTTCAGTCGAGAGAAAGGTTACG 430
Db 371 GCGTGTGTAAGAGAGCCCTTCGGGTTGTAAGCACTTTTGTCCGAGAAAGAAATCCTCTCG 430
QY 431 GTAATTAATCGTACTATGACGATGATGACAGAGAGACCGGCTTAATCTAGTCCAG 490
Db 431 GTTAATACCTCGGGGGGATGACGATGACCGGAAATAAGCACCGGCTTAATCTAGTCCAG 489
QY 491 CAGCCGCGGTAATAGTAGGGGTCAGAGGCTTAATCGGAAATTAATCGGGGTAAGAGGTCG 550
Db 490 CAGCCGCGGTAATAGTAGGGGTCAGAGGCTTAATCGGAAATTAATCGGGGTAAGAGGTCG 549
QY 551 CAGCGGCTTTGTAAGTACGATGATGAAATCCCGGGCTTAATCGTGGAAATTCGTTTAA 610
Db 550 CAGCGGCTTTGTAAGTACGATGATGAAATCCCGGGCTTAATCGTGGAAATTCGTTTAA 609
QY 611 ACTCAAGGCTTAAGTATGAGTGGGTCAGAGGAGGTAATTCGATGTAAGAGTAAATGCGT 670
Db 610 ACTCAAGGCTTAAGTATGAGTGGGTCAGAGGAGGTAATTCGATGTAAGAGTAAATGCGT 669
QY 671 AGAGATATGAGAAACATCGATGAGGAGGAGCGCTCTCGGTTAACTAGCGCTCAG 730
Db 670 AGAGATATGAGAAACATCGATGAGGAGGAGCGCTCTCGGTTAACTAGCGCTCAG 729
QY 731 CACGAAAGCGTGGGAGAGCAACAGATTAGATACCTGATAGTCCAGCCCTTAAACGATG 790
Db 730 CACGAAAGCGTGGGAGAGCAACAGATTAGATACCTGATAGTCCAGCCCTTAAACGATG 789
QY 791 TCAACTAGTGTGGGCTTTATTAGGCTTGTGTAAGCAAGCTAACGCGTGAAGTTGACCGC 850
Db 790 TCAACTAGTGTGGGCTTTATTAGGCTTGTGTAAGCAAGCTAACGCGTGAAGTTGACCGC 849
QY 851 CTGGGAGTACGTCGTCGCAAGATTAAACTCAAGAAATTGACGGGAGACCCGACAGGCG 910
Db 850 CTGGGAGTACGTCGTCGCAAGATTAAACTCAAGAAATTGACGGGAGACCCGACAGGCG 909
QY 911 TGAATTATGTGATTAATTTGATGACAGCGCAAAACCTTACCTTGCATGATGAC 970
Db 910 TGAATTATGTGATTAATTTGATGACAGCGCAAAACCTTACCTTGCATGATGAC 969
QY 971 GAAATTTCTAGAGATAGATTAGTGTCT--TCGGAAAGCTTAACAGAGTGTGATGCT 1027
Db 970 GAAATTTCTAGAGATAGATTAGTGTCT--TCGGAAAGCTTAACAGAGTGTGATGCT 1029
QY 1028 GTGTCAGTGTGTGTCGTAAGATTTGGGTTAAAGTCCCGCAACAGCGCAACCTTGTCA 1087
Db 1030 GTGTCAGTGTGTGTCGTAAGATTTGGGTTAAAGTCCCGCAACAGCGCAACCTTGTCC 1089
QY 1088 TTAATTTGCATCTTTGGTGGGCACTTAATGACATGCGGCTGACAAACCGAGGAG 1147
Db 1090 TTAATTTGC-----TAGCGAAGCACTTAAAGGAGATGCGGCTGACAAACCGAGGAG 1144
QY 1148 GTGGGATGACGTCAAGTCTCTATGACCCTTAATGGGTAAGGCTTCAACGTAATCAATG 1207
Db 1145 GTGGGATGACGTCAAGTCTCTATGACCCTTAATGGGTAAGGCTTCAACGTAATCAATG 1204
QY 1208 GCGGCTAAGAGGCTTGGCAACCGCGAGGGGAGCTAATCTCAAGAAAGCGGCTGTAGT 1267
Db 1205 GTCGCTAAGAGGCTTGGCAACCGCGAGGGGAGCTAATCTCAAGAAAGCGGCTGTAGT 1264
QY 1268 CCGGATCGGATCTGCACTGCACTCGTGAAGTGGATCGCTAGTATCGCGGATCAG 1327
Db 1265 CCGGATCGGATCTGCACTGCACTCGTGAAGTGGATCGCTAGTATCGCGGATCAG 1324
QY 1328 CATGTGCGGTGAATACGTTCCCGGCTTTGTAACACCGCCCTGACACCAATGGAGTG 1387
Db 1325 CATGTGCGGTGAATACGTTCCCGGCTTTGTAACACCGCCCTGACACCAATGGAGTG 1384
QY 1388 GGTTCACAGAGGATAGTCTTAACGCTAAGAGGCGCTGACAGGAGAT 1443
Db 1385 GGTTCACAGAGGATAGTCTTAACGCTAAGAGGCGCTTACACAGGAGAT 1440

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RESULT 5
US-09-617-854A-1
; Sequence 1, Application US/09617854A
; Patent No. 6461840
; GENERAL INFORMATION:
; APPLICANT: BRAMUCCI, MICHAEL G.
; APPLICANT: MCCUTCHEN, CAROL M.
; APPLICANT: NAGARAJAN, VASANTHA
; APPLICANT: THOMAS, STUART M.
; TITLE OF INVENTION: Microbial Production of Terephthalic Acid and
; TITLE OF INVENTION: Isophthalic Acid
; FILE REFERENCE: CL-1257
; CURRENT APPLICATION NUMBER: US/09/617, 854A
; CURRENT FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/091,645
; PRIOR FILING DATE: JULY 2, 1998
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 1
; LENGTH: 1451
; TYPE: DNA
; ORGANISM: Burkholderia sp.
US-09-617-854A-1

Query Match          76.0%; Score 1108; DB 3; Length 1451;
Best Local Similarity 87.2%; Pred. No. 0;
Matches 1252; Conservative 0; Mismatches 175; Indels 9; Gaps 3;

QY 11 GCGCGATGCTTTTACATGCAAGTCGACGCGACGAGATGCTTCATCTGTGGCGA 70
Db 11 GCGCGATGCTTTTACATGCAAGTCGACGCGACGAGATGCTTCATCTGTGGCGA 70
QY 71 GTGGCGGAGCGGTGACGTAATGCAATCCGGAACGTAATCCAGAGAGGGGGGTAAACGATGAA 130
Db 71 GTGGCGGAGCGGTGACGTAATGCAATCCGGAACGTAATCCAGAGAGGGGGGTAAACGATGAA 130
QY 131 AGATGTCTATAATCCGATATTAATCTTAAGAGAGAAACAGGGGATCGAAAGACCTTGGC 190
Db 131 AGCGGATTAATTAATCCGATATTAATCTTAAGAGAGAAACAGGGGATCGAAAGACCTTGGC 190
QY 191 TTTTGGAGCGCGCATGTCTGATTTAGCTGATGGTGGGTTAAAGGCTTACCAAGGCGACG 250
Db 191 TACAAAGACAGCGCATGTCAATTAATCTTGTGGTGGGTTAAAGGCTTACCAAGGCGACA 250
QY 251 ATCTGATGTTGTTGTGAGAGAGCAACGACCACTGAGACTGAGAACCGGCCAGCTC 310
Db 251 ATCTGATGTTGTTGTGAGAGAGCAACGACCACTGAGACTGAGAACCGGCCAGCTC 310
QY 311 CTACGGGAGGACAGAGTGGGGAATTTTGAACAATGGGCGCAAGGCTGATCCAGCAATGCC 370
Db 311 CTACGGGAGGACAGAGTGGGGAATTTTGAACAATGGGCGCAAGGCTGATCCAGCAATGCC 370
QY 371 GCGTGAATGAGAAAGGCTTCGAGTTGTAAAGCTCTTTCAGTCGAGAGAAAGGTTACG 430
Db 371 GCGTGTGTAAAGAAAGGCTTCGAGTTGTAAAGCACTTTTGTCCGAGAAAGAAATCCTCTCG 430
QY 431 GTAATTAATGTGACTATGACGATATGACAGAGAAAGCAACCGGCTTAATCTAGTCCAG 490
Db 431 GTTAATTAATCTCGGGGGATACGCTACCGGAAATAAGACCGGCTTAATCTAGTCCAG 489
QY 491 CAGCGGCGTAAATACGTAAGGAGTCAAGCGTTAAATCGGAATTAATCTGGGCGTAAAGGTCG 550
Db 490 CAGCGGCGTAAATACGTAAGGAGTCAAGCGTTAAATCGGAATTAATCTGGGCGTAAAGGTCG 549
QY 551 CAGCGGCTTTGTAAGTACGATGATGAAATCCCGGCTTAACTGGGAATTCGTTTAA 610
Db 550 CAGCGGCTTTGTAAGTACGATGATGAAATCCCGGCTTAACTGGGAATTCGTTTAA 609
QY 611 ACTCAAGGCTTAAGTATGAGTGGGTCAGAGGAGGTAATTCGATGTAAGAGTAAATGCGT 670
Db 610 ACTCAAGGCTTAAGTATGAGTGGGTCAGAGGAGGTAATTCGATGTAAGAGTAAATGCGT 669
QY 671 AGAGATATGAGAAACATCGATGAGGAGGAGCGCTCTCGGTTAACTAGCGCTCAG 730

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Db 670 AGGATGTGAGGAAATCCGATGCGGAGGAGCGCCCTGGCCAAATCTGACGCTATG 729
Qy 731 CACGAAAGCGTGGGAGCAAAACAGGATTAATACCTTGATGTCACGCCCTAAACGATG 790
Db 730 CACGAAAGCGTGGGAGCAAAACAGGATTAATACCTTGATGTCACGCCCTAAACGATG 789
Qy 791 TCAACTAGTTGTTGGGCTTATTAAGGCTTGTAACGAAAGCTAACGCTGAAGTTGACCGC 850
Db 790 TCAACTAGTTGTTGGGCTTATTAAGGCTTGTAACGAAAGCTAACGCTGAAGTTGACCGC 849
Qy 851 CTGGGGAGTACGCTGCGAAGATTAAACTCAAGAAATTAACGCGGAGCCGCAACAGCGG 910
Db 850 CTGGGGAGTACGCTGCGAAGATTAAACTCAAGAAATTAACGCGGAGCCGCAACAGCGG 909
Qy 911 TGAATTAATGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 970
Db 910 TGAATTAATGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 969
Qy 971 GAATTTTCTAGAGTATGATTAATGCT---TCGGGAGCGTAAACAGAGTGTGATGAGCT 1027
Db 970 GAATTTTCTAGAGTATGATTAATGCT---TCGGGAGCGTAAACAGAGTGTGATGAGCT 1029
Qy 1028 GTGTCAGCTCGTGTGTCGAGATGTTGGTTAAAGTCCGCAACAGCGCAACCTTGTC 1087
Db 1030 GTGTCAGCTCGTGTGTCGAGATGTTGGTTAAAGTCCGCAACAGCGCAACCTTGTC 1089
Qy 1088 TTAATTCGATCAATTTGGTGGGCACTTTAATGAGTCCCGGAGCAAAACGAGAGAG 1147
Db 1090 TTAATTCGATCAATTTGGTGGGCACTTTAATGAGTCCCGGAGCAAAACGAGAGAG 1144
Qy 1148 GTGGGGAGTACGCTCAAGTCTCAATGCGCTTAATGGGAGGCTTCAACGTAATCAATG 1207
Db 1145 GTGGGGAGTACGCTCAAGTCTCAATGCGCTTAATGGGAGGCTTCAACGTAATCAATG 1204
Qy 1208 GCGCGTACAGAGGAGTTCGCAACCGCGAGGAGGAGTAACTCAAGAAAGCGCTGTAAT 1267
Db 1205 GCGCGTACAGAGGAGTTCGCAACCGCGAGGAGGAGTAACTCAAGAAAGCGCTGTAAT 1264
Qy 1268 CCGGATCGAGTGTGCACTGCACTCGTGAATGCGAATGCGTGAATGCGGATCAG 1327
Db 1265 CCGGATCGAGTGTGCACTGCACTCGTGAATGCGAATGCGTGAATGCGGATCAG 1324
Qy 1328 CATGTGCGGCTGAATGCTCCGCGGCTTGTAACAACCGCGCTGCAACATGAGGAGT 1387
Db 1325 CATGTGCGGCTGAATGCTCCGCGGCTTGTAACAACCGCGCTGCAACATGAGGAGT 1384
Qy 1388 GGTTCACAGAGAGTGTGTAACCGTAAAGAGGAGCGCTTGCCACGCTGAGAT 1443
Db 1385 GGTTCACAGAGAGTGTGTAACCGTAAAGAGGAGCGCGCTTAACACGCGAGAGAT 1440

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RESULT 6  
US-08-642-229A-2  
Sequence 2, Application US/08642229A  
Patent No. 5874291

GENERAL INFORMATION:  
APPLICANT: Herwig, Russell P.  
APPLICANT: Bielefeldt, Angela R.  
APPLICANT: Stensel, H. David  
APPLICANT: Strand, Stuart E.  
TITLE OF INVENTION: Degradation of Environmental Toxins by a  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Christensen O'Connor Johnson and Kindness PLLC  
STREET: 1420 Fifth Avenue, Suite 2800  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: WA 98101-2347  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/642,229A
FILING DATE:
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/246,865
FILING DATE: 20-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sheiness, Diana K.
REGISTRATION NUMBER: 35,356
REFERENCE/DOCKET NUMBER: UOFW19233
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682 8100
TELEFAX: (206) 224 0779
TELEX: 4938023
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1452 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: nucleic acid
DESCRIPTION: "16S ribosomal DNA"
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Brachyomonas denitrificans AS-P1
US-08-642-229A-2

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Query Match 75.9%; Score 1105.6; DB 2; Length 1452;
Best Local Similarity 86.3%; Pred. No. 0; Mismatches 189; Indels 11; Gaps 3;
Matches 1260; Conservative 0;
Qy 1 ATTGAACGCTGGCGGATGCTTTTACATGCAAGTGAACGCGAGACGATGCTTCAT 60
Db 1 ATTGAACGCTGGCGGATGCTTTTACATGCAAGTGAACGCGAGACGATGCTTCAT 57
Qy 61 CTGTGCGCAGTGGCGGAGCGGAGTGAATGATCGGAAAGTATCCAGAAAGGCGGAT 120
Db 58 ATGCTGACGAGTGGCGAAAGCGGAGTGAATGATCGGAAAGTATCGGAGGAGAT 117
Qy 121 AGCATCGAAAGATGCTTAATACCGCATATCTTAAGAGAAAGCAAGGAGTCGAAA 180
Db 118 ACTACTCGAAAGAGTGGCTTAATACCGCATGAGACTGAGTTGAAGCGGAGACTTTG 177
Qy 181 GACCTTGCGCTTTGGAGCGCGGATGCTGATGCTGATGCTGATGCTGATGCTGATG 240
Db 178 GGCCTGCGCTTACTGAGCGCGGATGCTGATGCTGATGCTGATGCTGATGCTGATG 237
Qy 241 CAAGCGAGATCAATGATGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
Db 238 CAAGCGAGATCAATGATGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 297
Qy 301 GCCGAGACTCTTAACGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
Db 298 GCCGAGACTCTTAACGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 357
Qy 361 CAGCATGCGCGGTGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Db 358 CAGCATGCGCGGTGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 417
Qy 421 AAAGGTTACGTAATTAATGCTGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Db 418 AAAGGTTACGTAATTAATGCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 477
Qy 481 TACGTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Db 478 TACGTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 537
Qy 541 AAAGGTTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600

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Db 599 ACGGCTTTTGACCTGCAAGGCTGAGTGGCGGCAAGGGGATGGAATTCCTCCGCTGAC 658  
Qy 659 AGTAAATGCGTAGATATGGAAGAACATCGATGCGGCAAGGCGACCTCTGCGTTAA 718  
Db 659 AGTAAATGCGTAGATATGCGGAGGAGAACCGATGGCGAAGCAATCCCTGCGCTCA 718  
Qy 719 CTGAGCGTCAAGCAAGAGGTGGGAGCAAGAGTTGATCCCTGGAGTCCACG 778  
Db 719 CTGAGCGTCAAGCAAGAGGTGGGAGCAAGAGTTGATCCCTGGAGTCCACG 778  
Qy 779 CCTTAAAGATGTCAGTATGTTGGGCTTATTAAGCTGGTAAACGAACTAAAGCGGT 838  
Db 779 CCTTAAAGATGTCAGTATGTTGGGCTTATTAAGCTGGTAAACGAACTAAAGCGGT 838  
Qy 839 GAAGTTGACCGCTGGGAGTACGCTCGCAAGATTAAATCTCAAGAAATGACGCGGAC 898  
Db 839 GAAGTTGACCGCTGGGAGTACGCTCGCAAGATTAAATCTCAAGAAATGACGCGGAC 898  
Qy 899 CCGCAAGAGCGGTGATATGATGATTAATTCGATGCAAGCGGAAACCTTAAGCTACCC 958  
Db 899 CCGCAAGAGCGGTGATATGATGATTAATTCGATGCAAGCGGAAACCTTAAGCTACCC 958  
Qy 959 TTGACATGATGCAAGATTTTCTAGAGATAGATTAGCT---TCGGGAAAGCTTAAACAG 1015  
Db 959 TTGACATGATGCAAGATTTTCTAGAGATAGAGAGTCTCGAAAGAACTCGACACAG 1018  
Qy 1016 TGCTGATGCTGTCTGATGCTGCTGTGTGATGATGTTGGTTAACTCCGCAACGAGCG 1075  
Db 1016 TGCTGATGCTGTCTGATGCTGCTGTGTGATGATGTTGGTTAACTCCGCAACGAGCG 1078  
Qy 1076 CAACCTTGTATTAATGATGATGATGTTGGTGGGACCTTAAATGAGCTCCGCTGACA 1135  
Db 1076 CAACCTTGTATTAATGATGATGATGTTGGTGGGACCTTAAATGAGCTCCGCTGACA 1135  
Qy 1136 AACCGAGAGAGTGGGAGTACGTCAGTCTCACTGAGCTTAAAGTGGTAAAGGCTTACA 1195  
Db 1136 AACCGAGAGAGTGGGAGTACGTCAGTCTCACTGAGCTTAAAGTGGTAAAGGCTTACA 1195  
Qy 1134 AACCGAGAGAGTGGGAGTACGTCAGTCTCACTGAGCTTAAAGTGGGAGCTTACA 1193  
Db 1134 AACCGAGAGAGTGGGAGTACGTCAGTCTCACTGAGCTTAAAGTGGGAGCTTACA 1193  
Qy 1196 CGTAAATCAATGCGGCTGACAGAGGTTGCCAACCCGAGAGGAGGAGCTTAACTCAGAA 1255  
Db 1196 CGTAAATCAATGCGGCTGACAGAGGTTGCCAACCCGAGAGGAGGAGCTTAACTCAGAA 1253  
Qy 1256 GCGGCTGTAGTCCGAGTCCGAGTCTGCACTGCTCCGTAAGTCCGTAATCGTAACTA 1315  
Db 1256 GCGGCTGTAGTCCGAGTCCGAGTCTGCACTGCTCCGTAAGTCCGTAATCGTAACTA 1315  
Qy 1316 ATCGCGATCAGATGTCGCGGTGAATAGTTCCCGGCTTGTATCAACAGCCCGCTAC 1375  
Db 1316 ATCGCGATCAGATGTCGCGGTGAATAGTTCCCGGCTTGTATCAACAGCCCGCTAC 1373  
Qy 1376 AACATGAGAGTGGGTTTCAACAGAGAGGATGCTTAACTGTAAGAGAGGAGGCTTGCAC 1435  
Db 1376 AACATGAGAGTGGGTTTCAACAGAGAGGATGCTTAACTGTAAGAGAGGAGGCTTGCAC 1433  
Qy 1436 GGTAGATTCATGATGAGGCTG 1457  
Db 1436 GGTAGATTCATGATGAGGCTG 1455  
Db 1434 GGGCGGCTTGTGATGAGGCTG 1455

RESULT 9  
US-08-114-695A-8

Sequence 8, Application US/08114695A  
Patent No. 5508193  
GENERAL INFORMATION:  
APPLICANT: Mandelbaum, Raphael T.  
APPLICANT: Mackett, Lawrence P.  
TITLE OF INVENTION: DEGRADATION OF S-TRIAZINES IN SOIL AND  
TITLE OF INVENTION: WATER  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESS: SCHWEGMAN, LUNDBERG & WOESSNER, P.A.  
STREET: 3500 IDS CENTER

CITY: MINNEAPOLIS  
STATE: MN  
COUNTRY: USA  
ZIP: 55402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
FILING DATE: 31-AUG-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MUEITING, ANN M.  
REGISTRATION NUMBER: 33,977  
REFERENCE/DOCKET NUMBER: 600.268051  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612-339-0331  
TELEFAX: 612-339-3061  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1474 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: tRNA  
ORIGINAL SOURCE:  
ORGANISM: Pseudomonas cepacia  
US-08-114-695A-8

Query Match 75.1%; Score 1094.2; DB 2; Length 1474;  
Best Local Similarity 68.3%; Pred. No. 0;  
Matches 992; Conservative 248; Mismatches 203; Indels 9; Gaps 3;

Qy 1 ATGGAAGCTGCGCGGATGCTTACATGATGCAAGTCCAGCGG-C-AGCAGGATGCTTCA 59  
Db 28 AUNNAACGCTGGCGGCAAGGCTGUAUACCAUCCGAAACAUUCCUGUAGUGGGGCU 87  
Qy 60 TCTGTGGCGAGTGGCGGAGCGGTGATGATGATGCGAAAGCTATCCAAAGAGGCGGCT 119  
Db 88 ACCUGUGCGAGUGGCGCAAGCGGUGUAUACCAUCCGAAACAUUCCUGUAGUGGGGCU 147  
Qy 120 AACGATCGAAAGATGCTAATACGCGATATCTTAAGGAGAAAGAGGAGGATGAA 179  
Db 148 AGCAGCGCGAAAGCGGAAUUAUACCGCAUACGUAUCAAAGCGGAGGACCTG 207  
Qy 180 AGACCTTGGCTTTTGAAGCGGCGGATGCTGATTAAGTGGTGGGTTAAAGGCTTA 239  
Db 208 GGGGCTGCGGCUAAGGUGGCGGAGUGGCUAGUUAUACGUAUUGUGGGGUAAGGCTTA 267  
Qy 240 CCAAGCGAGATGATGATGCTTGAAGAGAGCAACGACCACTGAGGATGTAAGAC 299  
Db 268 CCAAGCGAGATGATGATGCTTGAAGAGAGCAACGACCACTGAGGATGTAAGAC 327  
Qy 300 GGGCGGACATCTTACGCGGAGGAGCGATGCTGATTAAGTGGTGGGTTAAAGCTGAT 359  
Db 328 GGGCGGACATCTTACGCGGAGGAGCGATGCTGATTAAGTGGTGGGTTAAAGCTGAT 387  
Qy 360 CCAAGATGCGCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 419  
Db 388 CCAAGATGCGCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 447  
Qy 420 AAAAGTTACGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 479  
Db 448 AAAUCCUGGCUUAUACAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 507  
Qy 480 CTAGTGGCGAGCGCGGCTTAAATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 539  
Db 508 CTAAGGCGAGCGCGGCTTAAATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 567  
Qy 540 TAAAGGCTGCGAGCGGCTTAAATGATGATGATGATGATGATGATGATGATGATGAT 599

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1 RESULT 10
2 US-09-735-567-6/c
3 ; Sequence 6, Application US/09735567
4 ; Patent No. 6608190
5 ; GENERAL INFORMATION:
6 ; APPLICANT: Bramucci, Michael
7 ; TITLE OF INVENTION: Nucleic Acid Fragments for the Identification of Bacteria in
8 ; TITLE OF INVENTION: Industrial Wastewater Bioreactors
9 ; FILE REFERENCE: BCI033 US NA
10 ; CURRENT APPLICATION NUMBER: US/09/735, 567

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| Query  | Match | Similarity  | Score | DB | Length | Matches | Mismatches | Indels | Gaps |
|--|-------|---|-------|----|--------|---------|------------|--------|------|
| <p>US-09-735-567-6</p> <p>Query Match 74.2%; Score 1080.8; DB 3; Length 1539;</p> <p>Best Local Similarity 85.7%; Pred. No. 0;</p> <p>Matches 1251; Conservative 0; Mismatches 197; Indels 12; Gaps 4;</p> |       |   |       |    |        |         |            |        |      |
| QY   | 3     | TGAACGCTGGCGGCATGCTTTACATATGCAATGCGAAGCGGACGACGATGCTTGATCT    | 62    |    |        |         |            |        |      |
| Db   | 1538  | TGAACGCTGGCGGCATGCTTTACATATGCAATGCGAAGCGGACGACGATGCTTGATCT    | 1481  |    |        |         |            |        |      |
| QY   | 63    | GGTGGCGAGTGGCGGAGCGGGTGAATATGATCGGAACGATACGAAGAGGGGGGTATAC    | 122   |    |        |         |            |        |      |
| Db   | 1480  | GGGGCGAGTGGCGGAGCGGGTGAATATGATCGGAACGATACGAAGAGGGGGGTATAC     | 1421  |    |        |         |            |        |      |
| QY   | 123   | GCATCGAAGATGTGCTAATATACCGCATATATCTTAAGAGAGAAAGCAGGGATC - GAAA | 180   |    |        |         |            |        |      |
| Db   | 1420  | TCGGCGAAGCGCGATTAATATCCGATGAGATCCGTGATGAAAAGCAGGGATCCGCAAG    | 1361  |    |        |         |            |        |      |
| QY   | 181   | GACCTTGGCGCTTTTGGAGCGCGCGATGTCTGATTTAGTACTTGTGGGTAAAGCCCTAC   | 240   |    |        |         |            |        |      |
| Db   | 1360  | GGCTTGGCGCTTCTGAGCGCGCGATGTCTGATTTAGTACTTGTGGGTAAAGCCCTAC     | 1301  |    |        |         |            |        |      |
| QY   | 241   | CAAGCGCAGCATAGTATGTGTCTGAGAGAGACGACCGACCACTGGGACTGAGACAG      | 300   |    |        |         |            |        |      |
| Db   | 1300  | CAAGCTCGCATCTGATAGTGTGTCTGAGAGAGATGATCAGCCATCGGAGCTGAGACAG    | 1241  |    |        |         |            |        |      |
| QY   | 301   | GCCCAAGCTCTTACCGGAGGACGATGGGGAATTTTGGACATGGCGCAAGCTGATC       | 360   |    |        |         |            |        |      |
| Db   | 1240  | GCCCAAGCTCTTACCGGAGGACGATGGGGAATTTTGGACATGGCGCAAGCTGATC       | 1181  |    |        |         |            |        |      |
| QY   | 361   | CACCAATGCCCGGTGATGAGAGAGCGCTTGGGTGTAAGCTCTTTCAGTCGAGAAGA      | 420   |    |        |         |            |        |      |
| Db   | 1180  | CACCAATGCCCGGTGATGAGAGAGCGCTTGGGTGTAAGCTCTTTCAGTCGAGAAGA      | 1121  |    |        |         |            |        |      |
| QY   | 421   | AAAGCTTACGTTAATATGATGACTCATGACGGTATCGACAGAGAGACCGGCTAAC       | 480   |    |        |         |            |        |      |
| Db   | 1120  | AAAGCTTACGTTAATATGATGACTCATGACGGTATCGACAGAGAGACCGGCTAAC       | 1061  |    |        |         |            |        |      |
| QY   | 481   | TACGTGCGACGACCGCGGTAAATACGATGGGTGCAAGCTTAAATCGAATTAATCTGGCGCT | 540   |    |        |         |            |        |      |
| Db   | 1060  | TACGTGCGACGACCGCGGTAAATACGATGGGTGCAAGCTTAAATCGAATTAATCTGGCGCT | 1001  |    |        |         |            |        |      |
| QY   | 541   | AAAGGTGGCGCAGCGCGCTTGTAAAGTACGATGTAAGTAATCCCGGCGCTTAACCTGGGAT | 600   |    |        |         |            |        |      |
| Db   | 1000  | AAAGGTGGCGCAGCGCGCTTGTAAAGTACGATGTAAGTAATCCCGGCGCTTAACCTGGGAT | 941   |    |        |         |            |        |      |
| QY   | 601   | TGCGTTTGAATCAAGAGCTAGAGTGTGCGACAGGAGGTGGAATTCATGTGTACAG       | 660   |    |        |         |            |        |      |
| Db   | 940   | TGCGTTTGAATCAAGAGCTAGAGTGTGCGACAGGAGGTGGAATTCATGTGTGTACAG     | 881   |    |        |         |            |        |      |
| QY   | 661   | TGAATATCGATGAGATATGGAAGAATGATGATGAGGAGGACGCTCTGGGTAAACACT     | 720   |    |        |         |            |        |      |
| Db   | 880   | TGAATATCGATGAGATATGGAAGAATGATGATGAGGAGGACGCTCTGGGTAAACACT     | 821   |    |        |         |            |        |      |
| QY   | 721   | GACGCTCATGACGAAAGCGTGGGAGCAAAACAGATTAGATACCTGTGATGTCACGCC     | 780   |    |        |         |            |        |      |
| Db   | 820   | GACGCTCATGACGAAAGCGTGGGAGCAAAACAGATTAGATACCTGTGATGTCACGCC     | 761   |    |        |         |            |        |      |
| QY   | 781   | CTTAAAGCATGCAATAGTTGTTGGCGCTTAATAGCTTGTATACGAAGCTTAACGCGTGA   | 840   |    |        |         |            |        |      |
| Db   | 760   | CTTAAAGCATGCAATAGTTGTTGGCGCTTAATAGCTTGTATACGAAGCTTAACGCGTGA   | 701   |    |        |         |            |        |      |

QY 841 AGTTGACCGCCCTGGGAGAGTACGGTCCGCAAGATTAAACTCAAGAAATTGACGGGACCC 900  
DB 700 AGTTACCGCCCTGGGAGAGTACGGGCGCAAGTTAAACTCAAGAAATTGACGGGACCC 641  
QY 901 GCACAGCGGCTGATGATGATGATTAATTCATGCAACGCAAAAACTTACCTACCTT 960  
DB 640 GCACAGCGGCTGATGATGATGATTAATTCATGCAACGCAAAAACTTACCTACCTT 581  
QY 961 GACATGACGCAATTTTCTAGAGATGATTAAGTCT--TCGGAAAGCTTAACAAGGTG 1017  
DB 580 GACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 521  
QY 1018 CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1077  
DB 520 CTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 461  
QY 1078 ACCCTTGTCAATTAATGCGATCATTTGTTGGGCACTTAAATGAGACTGCCGTGACAA 1137  
DB 460 ACCCTTGTCAATTAATGCGATCATTTGTTGGGCACTTAAATGAGACTGCCGTGACAA 406  
QY 1138 CCGAGAGAGGTGGGAGATGACGTCAAGTCTCATGAGCCCTTAATGGGTAGGCTTCAACG 1197  
DB 405 CCGAGAGAGGTGGGAGATGACGTCAAGTCTCATGAGCCCTTAATGGGTAGGCTTCAACG 346  
QY 1198 TAAATCAATGGGCGCTTACAGAGGCTTTCACACCCCGAGGGGAGCTAATCAAGAAAGC 1257  
DB 345 TCAATCAATGGGCGCTTACAGAGGCTTTCACACCCCGAGGGGAGCTAATCAAGAAAGC 286  
QY 1258 GCGTGTGATGCGGATCGGATCGGATCGGATCGGATCGGATCGGATCGGATCGGAT 1317  
DB 285 GCGTGTGATGCGGATCGGATCGGATCGGATCGGATCGGATCGGATCGGATCGGAT 226  
QY 1318 CCGGATCAAGATGTCGCGGTGATACGTTCCGGGTCTTTGACACACCGCCGTCAAC 1377  
DB 225 CCGGATCAAGATGTCGCGGTGATACGTTCCGGGTCTTTGACACACCGCCGTCAAC 166  
QY 1378 CATGGAGTGGGTTTACACAGAGAGAGTCTAATCCGTAAAGAGGGGGCTTTCACAGG 1437  
DB 165 CATGGAGTGGGTTTACACAGAGAGAGTCTAATCCGTAAAGAGGGGGCTTTCACAGG 106  
QY 1438 TGAATTCATGACTGGGGTG 1457  
DB 105 TGGGTTCTGACTGGGGTG 86

RESULT 11  
US-09-735-567-7  
Sequence 7, Application US/09735567  
Patent No. 6608190  
GENERAL INFORMATION:  
APPLICANT: Birmucel, Michael  
TITLE OF INVENTION: Nucleic Acid Fragments for the Identification of Bacteria in  
FILE REFERENCE: BC1033 US NA  
CURRENT APPLICATION NUMBER: US/09/735,567  
CURRENT FILING DATE: 2000-12-13  
PRIOR APPLICATION NUMBER: 60/171,140  
PRIOR FILING DATE: 16 DECEMBER 1999  
NUMBER OF SEQ ID NOS: 30  
SOFTWARE: Microsoft Office 97  
SEQ ID NO 7  
LENGTH: 1454  
TYPE: DNA  
ORGANISM: Unknown Organism  
FEATURES:  
OTHER INFORMATION: Description of Unknown Organism: Brachyomonas  
OTHER INFORMATION: Nucleotide sequence of the 16S rDNA corresponding to strain RA9  
US-09-735-567-7

Query Match 74.1%; Score 1080.2; DB 3; Length 1454;  
Best Local Similarity 85.6%; Pred. No. 0;  
Matches 1251; Conservative 0; Mismatches 198; Indels 12; Gaps 4;

QY 2 TTGAACGCTGGCGGATGCTTTACATGATGCAAGTCCGAGAGCAGGATGCTTGCATC 61  
DB 1 TTGAACGCTGGCGGATGCTTTACATGATGCAAGTCCGAGAGCAGGATGCTTGCATC 58  
QY 62 TGGTGGCAGTGGCGGAGCGGTTGATTAATGATGCAAGTATCCAGAGAGGGGGTAA 121  
DB 59 TGGTGGCAGTGGCGGAGCGGTTGATTAATGATGCAAGTATCCAGAGAGGGGGTAA 118  
QY 122 GCATCGAAGATGCTTAATACCGCATATACCTTAAGAGAGAAAGCAGGGGA--TCGAA 179  
DB 119 CTCGGCGAAGCCTGATTAATACCGCATATACCTTAAGAGAGAAAGCAGGGGA--TCGAA 178  
QY 180 AGACCTTGGCTTTTGGAGCGCGGATGCTTGAATGATGATGATGATGATGATGATGAT 239  
DB 179 GAGCTTGGCTTTTGGAGCGCGGATGCTTGAATGATGATGATGATGATGATGATGAT 238  
QY 240 CCAAGCGCAGATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 299  
DB 239 CCAAGCGCAGATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 298  
QY 300 GAGCCGATCTCTACGCGGAGCAGAGTGGGAAATTTGCAATGGGCGCAAGCTTAT 359  
DB 299 GAGCCGATCTCTACGCGGAGCAGAGTGGGAAATTTGCAATGGGCGCAAGCTTAT 358  
QY 360 CCAAGATGCGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 419  
DB 359 CCAAGATGCGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 418  
QY 420 AAAAGTTACCGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 479  
DB 419 AAAAGTTACCGTAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 478  
QY 480 CTACGTGCGACAGCGCGGATTAATACGATGATGATGATGATGATGATGATGATGAT 539  
DB 479 CTACGTGCGACAGCGCGGATTAATACGATGATGATGATGATGATGATGATGATGAT 538  
QY 540 TAAAGGTCGCGGAGCGGCTTTGTAAGTCAAGTGAATATCCCGGGCTTAACTGGGAA 599  
DB 539 TAAAGGTCGCGGAGCGGCTTTGTAAGTCAAGTGAATATCCCGGGCTTAACTGGGAA 598  
QY 600 TTGCGTTGAAACTCAAGGCTAAGTGTGGCAGAGGAGTGAATTCATGATGATGAT 659  
DB 599 TTGCGTTGAAACTCAAGGCTAAGTGTGGCAGAGGAGTGAATTCATGATGATGAT 658  
QY 660 GTGAATGCGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 719  
DB 659 GTGAATGCGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 718  
QY 720 TGAAGCTTCAAGCAAGAAAGCTGGGAGCAACAGATTAATACCTGATGATGATGAT 779  
DB 719 TGAAGCTTCAAGCAAGAAAGCTGGGAGCAACAGATTAATACCTGATGATGATGAT 778  
QY 780 CCTAAAGATGCAACTAGTTGTTGGGCTTAAATGATGATGATGATGATGATGATGAT 839  
DB 779 CCTAAAGATGCAACTAGTTGTTGGGCTTAAATGATGATGATGATGATGATGATGAT 838  
QY 840 AAGTTGACCGCTGGGAGTACGCTGCCAAGATTAATCAAGAAATTGACGGGAGC 899  
DB 839 AAGTTGACCGCTGGGAGTACGCTGCCAAGATTAATCAAGAAATTGACGGGAGC 898  
QY 900 CCGCAAGCGGTGATTAATGATGATTAATTCGATGCAACGGAAGAACTTACCTACCT 959  
DB 899 CCGCAAGCGGTGATTAATGATGATTAATTCGATGCAACGGAAGAACTTACCTACCT 958  
QY 960 TGAATGATGCAATTTTCTAGAGATGATTAAGTCT--TCGGGAAGCTTAACAAGGT 1016  
DB 959 TGAATGATGCAATTTTCTAGAGATGATTAAGTCT--TCGGGAAGCTTAACAAGGT 1018  
QY 1017 GCTGATGCTGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1076  
DB 1019 GCTGATGCTGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1078

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QY 1077 AACCTTGTCAATTAATGTCATTTGGTGGCACTTAAATGAGCTGCGGTGACAA 1136
DB 1079 AACCTTGTCAATTAATGTCATTTGGTGGCACTTAAATGAGCTGCGGTGACAA 1133
QY 1137 ACCGGAAGAGGTGGGAGTACAGTCTCAAGTCTTCATGAGCCCTTAATGAGGCTTCAAC 1196
DB 1134 ACCGGAAGAGGTGGGAGTACAGTCTCAAGTCTTCATGAGCCCTTAATGAGGCTTCAAC 1193
QY 1197 GTAAATCAATGAGGCTGACAGAGGTTGCAACCCCGAGGGGAGCTAATCTCAAGAA 1256
DB 1194 GTCAATCAATGAGGCTGACAGAGGTTGCAACCCCGAGGGGAGCTAATCTCAAGAA 1253
QY 1257 CCGGTGTAGTCCGAGTCCGAGTCTGCAACTCCGTAAGTCCGTAAGTCTGTA 1316
DB 1254 CCGGTGTAGTCCGAGTCCGAGTCTGCAACTCCGTAAGTCCGTAAGTCTGTA 1313
QY 1317 TCGCGATCAGCAATGTCGCGGTGAATACGTTCCGGGTCTTGTACACACCGCCGTACA 1376
DB 1314 TCGTGATCAGCAATGTCGCGGTGAATACGTTCCGGGTCTTGTACACACCGCCGTACA 1373
QY 1377 CCATGGAGTGGGTTTCAACCAAGAGTACTTAACCGTAAAGAGGGGCTTGGCAAG 1436
DB 1374 CCATGGAGCGGGTTCACCAAGAGTACTTAACCGTAAAGAGGGGCTTGGCAAG 1433
QY 1437 GTGAGATTCATGACTGGGGTG 1457
DB 1434 GTGGGTTCTGACTGGGGTG 1454

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## RESULT 12

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US-09-735-567-2/c
Sequence 2, Application US/09735567
Patent No. 6508190

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GENERAL INFORMATION:
APPLICANT: Bramucci, Michael
TITLE OF INVENTION: Nucleic Acid Fragments for the Identification of Bacteria in
FILE REFERENCE: BC1033 US NA
CURRENT APPLICATION NUMBER: US/09/735,567
CURRENT FILING DATE: 2000-12-13
PRIOR APPLICATION NUMBER: 60/171,140
PRIOR FILING DATE: 16 DECEMBER 1999
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Microsoft Office 97
SEQ ID NO: 2
LENGTH: 1467
TYPE: DNA
ORGANISM: Unknown Organism
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: Brachymonas
OTHER INFORMATION: Nucleotide sequence of 16S rDNA corresponding to strain NBE13
US-09-735-567-2

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Query Match 74.1%; Score 1079.6; DB 3; Length 1467;
Best Local Similarity 85.6%; Pred. No. 0;
Matches 1251; Conservative 0; Mismatches 199; Indels 12; Gaps 4;

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QY 1 ATTTGAACGCTGGCGGCAATGCTTTACATGCAAGTGAACGGGACGAGCTTGCAAT 60
DB 1465 ATTTGAACGCTGGCGGCAATGCTTTACATGCAAGTGAACGGGACGAGCTTGCAAT 1408
QY 61 CTGGTGGCGAGTGGCGGAGGAGTGAATGATCGGAAAGTATCCAGAAAGAGGGGGTA 120
DB 1407 ATGGCGGCGAGTGGCGGAGGAGTGAATGATCGGAAAGTATCCAGAAAGAGGGGGTA 1348
QY 121 ACGCATCGAAGATGTGTAATATCCGATATATCTTAAGAGAGGAAAGAGGGGA--TCGA 178
DB 1347 GCTCGGCGAAGCGGAGTATTAATCCGATGATTCGTGATGAAGAGCGGGGACTCGCA 1288
QY 179 AAGACTTTCGCTTTTGGAGCGGCGGATGCTGATTAAGCTAGTTGGTGGGTAAAGGCT 238
DB 1287 AAGGCTTTCGCTTTCGAGAGCGGCGGATGCTGATTAAGCTAGTTGGTGGGTAAAGGCT 1228

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QY 239 ACCAAGCGCAGCATGATGTTGTTCTGAGAGAGCAGACCGCAACCTGGGACTGAGACA 298
DB 1227 ACCAAGCTGCGATCTGTAGTCTGATGAGAGAGATGATGAGCAATCGGGACTGAGACA 1168
QY 299 CGGCCGAGCTCTTACCGGAGGACGACAGTGGGAAATTTTGACAAATGGCGGACCTGA 358
DB 1167 CGGCCGAGCTCTTACCGGAGGACGACAGTGGGAAATTTTGACAAATGGCGGACCTGA 1108
QY 359 TCCACCAATGCGCGGTGAGTGAAGAGCTTCGGGTTGTAAGCTCTTCACTGAGGAA 418
DB 1107 TCCACCAATGCGCGGTGAGTGAAGAGCTTCGGGTTGTAAGCTCTTCACTGAGGAA 1048
QY 419 GAAAAGTTACCGTAAATATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTA 478
DB 1047 GAAAAGCTCTTCTTAATTAAGAGGCAATGACGTAACCGTAATTAAGCAACGGGCTA 988
QY 479 ACTAGTGCACAGACCGCGGTGAATACGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 538
DB 987 ACTAGTGCACAGACCGCGGTGAATACGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 928
QY 539 GTAAAGGGTGGCGGAGCGGCTTGTAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 598
DB 927 GTAAAGGGTGGCGGAGCGGCTTGTAAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 868
QY 599 ATTGCGTTGAAACTACAAAGCTAGAGTGGGACAGAGGAGTGAATTCATGTTGTAAC 658
DB 867 ACTGCGATTTGTAATGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 808
QY 659 AGTGAATGCGTAGATATGAGAGAACATCGATGCGGAGCGAGCTCTTGGGTTACA 718
DB 807 AGTGAATGCGTAGATATGAGAGAACATCGATGCGGAGCGAGCTCTTGGGTTACA 748
QY 719 CTGACGCTCAGTACAGAAAGCGTGGGAGCAACAGATGCGAAGCGAAGCTCTTGGGTTACA 778
DB 747 CTGACGCTCAGTACAGAAAGCGTGGGAGCAACAGATGCGAAGCGAAGCTCTTGGGTTACA 688
QY 779 CCTTAAAGATGTAATGTAAGTGGGCTTATTAAGCTTGTGAACGAAAGCTTAACGCT 838
DB 687 CCTTAAAGATGTAATGTAAGTGGGCTTATTAAGCTTGTGAACGAAAGCTTAACGCT 628
QY 839 GAAAGTTACCGCTTGGGAGTACGCTCGGAGATTAATTAATTAATTAATTAATTAATTA 898
DB 627 GAAAGTTACCGCTTGGGAGTACGCTCGGAGATTAATTAATTAATTAATTAATTAATTA 568
QY 899 CCGCAAGCGGTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 958
DB 567 CCGCAAGCGGTGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 508
QY 959 TTGACATGATGCAATTTTCTAGAGATGATTAAGTCT--TCGGGAAAGCTTAACAGAG 1015
DB 507 TTGACATGATGCAATTTTCTAGAGATGATTAAGTCT--TCGGGAAAGCTTAACAGAG 448
QY 1016 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1075
DB 447 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 388
QY 1076 CAACCTTGTCAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1135
DB 387 CAACCTTGTCAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 333
QY 1136 AACCGGAAGAGTGGGAGTACGTAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCA 1195
DB 332 AACCGGAAGAGTGGGAGTACGTAAGTCTCAAGTCTCAAGTCTCAAGTCTCAAGTCTCA 273
QY 1196 CGTAATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1255
DB 272 CGTAATTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 213
QY 1256 GCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1315
DB 212 GCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 153
QY 1316 ATGCGGATCAGCATGTCGCGGTGAATACGTTCCGGGTCTTGTACACACCGCCGCTAC 1375

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| Accession | Sequence  | Position |
|-----------|---|----------|
| Db        | 152 ATCTGGATCAGCAGCTCAGCGTAGATAGCTCCCGGGCTTGTACACACCGCCCTGCAC   | 93       |
| Oy        | 1376 ACCATGGAGTGGGGTTTCAACGAGACAGTATGTTAAACCTAAGAGAGGCGCTTGCCAC | 1433     |
| Db        | 92 ACCATGGAGGCGGGTCTACCAACGACAGGTGCTTAAACCGACAGAGGCGCTTGCCAC    | 33       |
| Oy        | 1436 GGTGAGATTCAATGACTGGGGTG                                    | 1457     |
| Db        | 32 GGTGGGAGTTCGTGACTGGGGTG                                      | 11       |

RESULT 13  
US-09-063

Sequence 1, Application US/09063898  
Patent No. 6319497

GENERAL INFORMATION:

APPLICANT: Caside, Jr., Lester B.  
APPLICANT: Falkinham, III, Joseph Oliver  
TITLE OF INVENTION: NON-OBLIGATE PREDATORY BACTERIUM  
TITLE OF INVENTION: BURGOLDERIA CASIDAE AND USES THEREOF  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1667 K Street, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20006

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 2.0

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/063,898  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/004,532  
FILING DATE: 23-APR-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Mastrock, Leslie  
REGISTRATION NUMBER: 18,872  
REFERENCE/DOCKET NUMBER: 8743-006-999  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)79990930  
TELEFAX: (212)869741  
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1495 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown

MOLECULE TYPE: Genomic DNA

US-09-063-898-1

|                            |       |                 |            |              |
|----------------------------|-------|-----------------|------------|--------------|
| Query Match                | 72.8% | Score 1060.8;   | DB 3;      | Length 1495; |
| Best Local Similarity      | 86.6% | Pred. No. 0;    |            |              |
| Matches 1264; Conservative | 0;    | Mismatches 182; | Indels 14; | Gaps 8       |

QY 1 ATTGAAGCGCTGGCGGAGATGCTTTAA-CATGGAAGTCGAACGGCAGCAGCGATGCTTGA 59  
Db 3 AATTACGCTGGTTGATGCTTTACGACATGAGTCGAACGGCAGCAGCGGCTCTTGA 62  
QY 60 TCTGATGGCGAGTGGCGGACGGGTGATGATCATCGAAC-GTATCCGAAGAAGGGGGG 118  
Db 63 CCTGGTGGCGAGTGGCGGAACGGGTGATGATCATCGGAACAATGTCCTGTAAGGGGGA 122  
QY 119 TACCGATCGAAGAATGTGCTAATACCGATATCTTAAGAGGAAGAAGCGGGGATCGA 178

[illegible]







QY 1371 GTGACACCATGGGAGTGGGTTTTCACCAAGACGTAAGTCTAACCGTTAAGAGGGCCCTT 1430  
 Db 1404 GTGACACCATGGGAGTGGGTTTTCACCAAGACGTAAGTCTTAACCGTAAGAGGGGGCCCTT 1463  
 QY 1431 GCCACGGTGAGATTCAATGACTGGGGTG 1457  
 Db 1464 GCCACGGTGAGATTCAATGACTGGGGTG 1490

Search completed: April 6, 2006, 21:34:17  
 Job time : 257 secs

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